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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/13, C07K 16/44, 19/00, C12N 15/62, G01N 33/577, 33/53, C12N 5/20		A1	(11) International Publication Number: WO 96/39518 (43) International Publication Date: 12 December 1996 (12.12.96)
(21) International Application Number: PCT/US96/09258 (22) International Filing Date: 5 June 1996 (05.06.96) (30) Priority Data: 08/462,798 5 June 1995 (05.06.95) US 08/541,373 10 October 1995 (10.10.95) US (60) Parent Applications or Grants (63) Related by Continuation US 08/541,373 (CIP) Filed on 10 October 1995 (10.10.95) US 08/462,798 (CIP) Filed on 5 June 1995 (05.06.95) (71) Applicant (for all designated States except US): BIONE-BRASKA, INC. [US/US]; 3820 Northwest 46th Street, Lincoln, NE 68524 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): WYLIE, Dwane, E. [US/US]; 5641 Hickory Crest Road, Lincoln, NE 68516 (US). LOPEZ, Osvaldo [AR/US]; 8210 North Hazlewood Drive, Lincoln, NE 68506 (US). MURRAY, Peter, Joseph [US/US]; 15417 "Y" Street, Omaha, NE 68137 (US).		(74) Agent: BRUESS, Steven, C.; Merchant, Gould, Smith, Edell, Welter & Schmidt, 3100 Norwest Center, 90 South Seventh Street, Minneapolis, MN 55402 (US). (81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: LEAD BINDING POLYPEPTIDES AND NUCLEOTIDES CODING THEREFOR			
(57) Abstract <p>Metal binding polypeptides which include an amino acid sequence coding for a variable region of a monoclonal antibody which immunoreacts with a lead cation and nucleotides which include a nucleic acid sequence coding for the variable region are provided. The invention is also directed to fusion proteins which include the monoclonal antibody heavy chain variable region and a phage coat protein or portion thereof. The invention also provides bacteriophages which include the fusion protein in their coat. In addition, methods for detecting, removing, adding, or neutralizing lead cations in biological or inanimate systems through the use of the lead binding polypeptides are provided. A method of forming a hybridoma which produces monoclonal antibodies capable of immunoreacting with a metallic cation is also provided.</p>			

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**LEAD BINDING POLYPEPTIDES AND
NUCLEOTIDES CODING THEREFORE**

Background of the Invention

5 Small chemical moieties, such as heavy metal ions, can and often do affect the environment and biological systems. These effects become astounding when it is realized that minute quantities of these small moieties are involved. Moreover, the presence or absence of low
10 concentrations of small moieties in the environment can have long term consequences. Minute quantities of metallic cations, such as lead cations, can regulate, influence, change or toxify the environment or biological systems.

15 The detection, removal, addition or neutralization of such minute quantities constitutes a focal point for continued research in many fields. For example, many efforts have been made to detect and remove minute, toxic amounts of heavy metal ions such as lead or
20 mercury from the environment. The efforts often have not been successful or economical for widespread application. On the other hand, minute concentrations of other heavy metals are important for the proper function of biological organisms. Zinc, for example,
25 plays a major role in wound healing.

 Heavy metal can exhibit dual roles. For example, lead is used in glass making and in chemical manufacturing operations. Yet when ingested by mammals, such as from drinking water, lead may be highly toxic in
30 very small amounts. Hence, detection and quantification of minute concentrations of a heavy metal, such as lead, in drinking water and other media would serve exploratory, safety and regulatory goals.

 It would, therefore, be highly desirable to
35 identify and control minute quantities of heavy metals, e.g., lead cations, in aqueous biological or inanimate systems. In most contexts, however, the detection, removal, addition or neutralization of heavy metals, is a difficult and expensive and often unfeasible if not

impossible task. Other metallic contaminants often mimic the heavy metal of interest and result in measurement interference. Moreover, the detection methods employed today are usually not sufficiently sensitive at the minute quantities under consideration. Consequently, it is desirable to develop reliable and economic methods for accurately identifying and controlling minute quantities of a particular heavy metal in the presence of other heavy metals.

Antibodies would seem to be uniquely suited for this task. Their high degree of specificity for a known antigen would avoid the potential interference caused by contaminants. The sensitivity of antibodies in assays to detect analytes in the picomolar or lower range would permit accurate and efficient targeting and detection at minute levels.

Monoclonal antibodies, of course, come to mind as especially suited agents for practice of this technique. Since Kohler and Milstein published their article on the use of somatic cell hybridization to produce monoclonal antibodies (Nature 256:495 (1974)), immunologists have developed many monoclonal antibodies which strongly and specifically immunoreact with antigens.

Notwithstanding this suggestion, the conventional understanding about immunology teaches that antibodies against small moieties, such as heavy metals, cannot be developed. The mammal immunization step, which is key for the production of monoclonal antibodies, typically requires a molecule that is large enough to cause antigenic reaction. Medium sized molecules (haptens), which are not of themselves immunogenic, can induce immune reaction by binding to an immunogenic carrier. Nevertheless, immunologists view small moieties such as metallic cations, as not large or structurally complex enough to elicit an antibody response. The molecular size and lack of complexity of an inorganic cation is

thought to render it insufficient for eliciting an antibody response.

Several immunologists have reported production of monoclonal antibodies to metallic ion chelates. For example, in U.S. Patent No. 4,722,892, monoclonal antibodies are disclosed which immunoreact with a complex of a chelating agent, such as ethylene diamine tetracetate (EDTA), and a heavy metal such as indium. In EPO Patent Application 0235457, monoclonal antibodies that immunoreact with cyanide complexes of gold and/or silver are disclosed. In these instances, however, the monoclonal antibodies bind with the metal chelate complex rather than the bare metallic ion itself. Disadvantages of antigen measurement methods based on such antibodies include: the complicated reagents involved in detection, lack of simple tests that discriminate among antigens, cross-reactivity with chelates of other antigens and cross-reactivity with the chelating agent itself.

Other instances of monoclonal antibody combinations with metals involve metal tags. The metals or metal chelates are bound to the antibody at a site remote from the antigen binding site or sites. The metal tag is not the antigen. Instead, the metal tag is used to indicate the presence of the monoclonal antibody when it reacts with its specific antigen. See for example, V.P. Torchilian et al., Hybridoma, 6, 229 (1987); and C.F. Meares, Nuclear Medical Biology, 13, 311-318 (1986).

Accordingly, there exists a need to develop polypeptides that immunoreact with heavy metals per se and with lead ions in particular. This would permit the development of methods for detecting or neutralizing heavy metals within, adding heavy metals to, or removing heavy metals from biological or inanimate systems through the use of the monoclonal antibodies. There also exists a need for the development of nucleic acid sequences coding for polypeptides which selectively bind

with lead cations and the development of methods of expressing and translating these nucleic acid sequences to produce metal binding polypeptides.

5

Summary of the Invention

The present invention provides a metal binding polypeptide which selectively binds a heavy metal, such as a lead cation. The metal binding polypeptide includes an amino acid sequence for a variable region
10 from a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation. For example, the metal binding polypeptide may include an amino acid sequence for a heavy chain Fd fragment (consisting of the heavy-chain variable region and heavy-chain constant
15 region 1 domains) from the monoclonal antibody. The metal binding polypeptide may further include a heavy chain Fc fragment fused to the heavy chain Fd fragment or a phage coat protein or portion thereof fused to the heavy chain Fd fragment. Alternatively, the metal
20 binding polypeptide may include an amino acid sequence for a light chain from the monoclonal antibody.

Another embodiment of the invention provides a recombinantly produced Fab fragment that immunoreacts with a lead cation. The recombinantly produced Fab
25 fragment includes an amino acid sequence for a variable region from a monoclonal antibody which immunoreacts with the lead cation. Preferably, the Fab fragment includes a heavy chain Fd fragment or a light chain from the monoclonal antibody.

30 The present invention also provides a purified antibody which includes a Fab fragment. The Fab fragment immunoreacts with a lead cation and includes an amino acid sequence selected from a group of sequences for a variable region of certain specified monoclonal
35 antibodies. The Fab fragment heavy chain preferably includes an amino acid sequence selected from a group of the sequences for the heavy chain variable region of the

specified monoclonal antibodies. In another preferred embodiment, the Fab fragment light chain includes an amino acid sequence selected from a group of the sequences for the light chain variable region of the specified monoclonal antibodies. The monoclonal antibody may be a recombinantly produced monoclonal antibody.

The invention is also directed to a heavy chain of the monoclonal antibody. The heavy chain preferably includes a sequence selected from a group of the sequences for the heavy chain variable region of certain specified monoclonal antibodies. The invention is also directed to a light chain of the monoclonal antibody. As with the heavy chain, the light chain preferably includes a sequence selected from a group of the sequences for the light chain variable region of certain specified monoclonal antibodies.

Yet another embodiment of the invention is directed to an isolated nucleic acid sequence coding for a variable region of a monoclonal antibody, e.g., the heavy chain variable region or the light chain variable region of the monoclonal antibody. The monoclonal antibody immunoreacts with a lead cation. Alternatively, the isolated nucleic acid sequence may code for the heavy chain Fd fragment, the entire heavy chain or the entire light chain of the monoclonal antibody.

The present invention is also directed to an expression cassette. The expression cassette includes a nucleic acid sequence coding for a variable region of the monoclonal antibody which immunoreacts with a lead cation. The nucleic acid sequence coding for the variable region is operably linked to a promoter functional in a vector. The expression cassette may include the promoter operably linked to a nucleic acid sequence coding for a heavy chain Fd fragment of the monoclonal antibody. Alternatively, the expression

cassette may include the promoter operably linked to a nucleic acid sequence coding for a light chain of the monoclonal antibody. The expression cassette may also include a leader sequence located between the promoter
5 and the nucleic acid sequence coding for the monoclonal antibody chain. The leader sequence may function to direct the heavy or light chain to a membrane in a host cell or to cause the antibody chain to be secreted by the host cell.

10 In another embodiment, the present invention provides a fusion protein which includes a phage coat protein or portion thereof fused to an amino acid sequence for a heavy chain variable region from the monoclonal antibody. The fusion protein preferably
15 includes the heavy chain Fd fragment of the monoclonal antibody. The fusion protein may be present as part of the coat of a phage and, preferably, the coat of a filamentous phage.

Another embodiment of the present invention is
20 directed to an expression cassette coding for a fusion protein. This expression cassette includes a first nucleic acid sequence coding for a heavy chain Fd fragment of a monoclonal antibody which reacts with a lead cation. The first nucleic acid sequence is linked
25 for co-expression to a second nucleic acid sequence, such as a nucleic acid sequence coding for a phage coat protein or a portion thereof, to form a nucleic acid sequence encoding the fusion protein. The fusion protein includes the heavy chain Fd fragment fused to
30 the phage coat protein or portion thereof. The expression cassette coding for the fusion protein also includes a promoter that is functional in a vector. The promoter is operably linked to the first and second DNA sequences and provides for expression of the fusion
35 protein. The expression cassette may also include a leader sequence which directs expression of the fusion protein to a membrane of a host cell. The leader

sequence is located between the promoter and the nucleic acid sequence coding for the fusion protein. In addition, the expression cassette may include a third nucleic acid sequence coding for a peptide linker. The
5 third nucleic acid sequence is typically located between the first and second nucleic acid sequences. The expression cassette may optionally include a fourth nucleic acid sequence coding for a light chain of a monoclonal antibody. Preferably, the light chain is a
10 light chain of a monoclonal antibody that immunoreacts with a lead cation. The present invention also provides a phagemid vector which includes one of the expression cassettes described above.

The invention is also directed to methods for
15 detecting, removing, adding, or neutralizing the heavy metals in biological and inanimate systems through the use of the metal binding polypeptides, heavy and light chains, fusion proteins, recombinantly produced Fab fragments and monoclonal antibodies described above.

20 The advantages of the invention include among others: the lack of complication by additional reagents, a high discrimination against similar metallic cations, lack of cross-reactivity with similar metallic cations, and lack of cross-reactivity with test
25 reagents.

The metal binding polypeptide of the invention binds with a heavy metal per se, and preferably with a lead cation per se. The metal binding polypeptide binds with a heavy metal cation which is at least partially
30 exposed, i.e., a heavy metal cation which is not complexed or enveloped. For example, the heavy metal cation may be associated with a spacer arm which includes a sulfur atom as a Lewis base group. The state of the heavy metal during the immunoreaction is
35 preferably one of non-coordination with any other substance; in other words, bare or exposed.

Preferably, the metal binding polypeptide exhibits a substantially high degree of specific immunoreactivity toward the heavy metal. More preferably, the metal binding polypeptide includes a portion of a

5 recombinantly produced Fab fragment (e.g., the light chain or the heavy chain Fd fragment of the Fab fragment) and has an association constant for a heavy metal such as a lead cation that is about 10,000 fold greater than the association constant for the immunogen

10 compound without the heavy metal. Also preferably, the metal binding polypeptide is immunospecific for a particular member of a group of very similar heavy metals. The monoclonal antibody will typically exhibit a relative association constant for such a particular

15 heavy metal that is about 10,000 fold greater than that for the other heavy metals of such a group.

The hybridoma of the invention, which produces the monoclonal antibody, is formed from immune cells that are specific for the heavy metal. The formation may be

20 accomplished by fusion of an immortal mammal cell line and mammalian immune cells from a second mammal previously immunized with an immunogen compound which contains the heavy metal. A lead cation monoclonal antibody produced by this first type of hybridoma is

25 hereinafter referred to as a "Group 1 lead cation monoclonal antibody." Alternatively, the hybridoma may be formed by fusion of an immortal mammal cell line and mammalian immune cells from a second mammal previously immunized with a second monoclonal antibody capable of

30 immunoreacting with the heavy metal. A lead cation monoclonal antibody produced by this latter type of hybridoma is hereinafter referred to as a "Group 3 lead cation monoclonal antibody." Selection of the appropriate hybridoma may be carried out by cross-

35 screening the secreted monoclonal antibody against the heavy metal and against controls.

The immunogen compound of the invention is typically composed of a biopolymer carrier, a spacer arm covalently bonded to the carrier and the heavy metal coordinated to the spacer arm. The spacer arm is
5 preferably semi-rigid and has at least one heavy metal coordination site. This arrangement maintains the heavy metal in at least a partially exposed state and prevents substantially complete inclusion or chelation of the heavy metal by spacer arm and/or carrier. The
10 biopolymer carrier may be a polysaccharide, a synthetic polyamide or preferably a protein. Preferred classes include blood or tissue sera proteins.

The spacer arm is generally no more than about 25 atoms in length. Preferably, the spacer arm is composed
15 of one of three classes: an oligopeptide, an aliphatic compound or an aliphatic fragment. More preferably, the spacer arm is an oligopeptide. The first two classes are generally each substituted with no more than about 2 pendent Lewis acid or base groups, and a coupling group
20 for forming a covalent bond with the protein carrier. The aliphatic fragment is substituted by a coupling group for forming a covalent bond with the protein carrier, and a carboxylic acid, hydroxyl, mercapto, amine or other group adapted for interacting with the
25 heavy metal. For each class of spacer arm, the coupling group is an amine, carboxylic acid, aldehyde, hydroxyl or mercapto group.

A preferred spacer arm for metallic cations is an oligopeptide or aliphatic compound having no more than
30 about 2 pendent Lewis base groups wherein the deformation of the electron shell of the Lewis base group is approximately of the same character as the deformation of the electron shell of the metallic cation. Especially preferred Lewis base groups for
35 transition elements and the heavy metals are those containing sulfur, such as a sulfonate or thiol group. Especially preferred are spacer arms which include

glutathione and cysteine, mercapto ethanol amine, dithiothreitol, amines and peptides containing sulfur, and the like. Other preferred spacer arms include a carboxylic acid group or a phosphorus-containing Lewis
5 base group such as a phosphonate anion.

The metallic cations are derived from metals such as period four transition metals, and period five, six and seven metals, transition elements and inner
10 transition elements. The metallic cations of special mention as the heavy metal include those derived from zinc, lead, cadmium, bismuth, cobalt, arsenic, chromium, copper, nickel, strontium and mercury. Preferably, the metallic cations are lead cations, e.g., lead(II) cations.

15 The present invention also provides a method of forming a hybridoma which produces an antibody capable of immunoreacting with a lead cation and preferably with an exposed form of the lead cation. The method includes inoculating a mammal with a solution containing second
20 antibodies which are capable of immunoreacting with the lead cation. Immune cells are isolated from the mammal and fused with an immortal mammal cell line from a second mammal. The resulting fused cell lines are selected for hybridomas which produce monoclonal
25 antibodies capable of immunoreacting with a lead cation (Group 3 lead cation monoclonal antibodies; "Group 3 Pb mAbs").

Methods according to the invention utilize the metal binding polypeptide for detection, removal,
30 neutralization or addition of the heavy metal respectively in, from, within or to a solid, liquid or gaseous medium. These methods utilize features such as metal binding polypeptide immobilization, heavy metal immobilization, competitive binding, and means employing
35 an oscillating probe, a micromagnetic probe and other physiochemical methods typically used to monitor antigen-antibody interactions.

Methods for detection that are based upon heavy metal immobilization may indicate the presence of the heavy metal-metal binding polypeptide conjugate (e.g., a lead cation-Fab fragment conjugate) by known immunologic assay techniques. In a first step, the heavy metal may be coordinated with an immobilized spacer arm. The spacer arm can be any of the foregoing that will hold the heavy metal in at least a partially exposed state. It need not be the same spacer arm of the immunogen compound used to develop the metal binding polypeptide. Non-immobilized materials are then removed from the mixture holding the immobilized spacer arm-heavy metal. Addition of the metal binding polypeptide (e.g., Fab fragment), removal of uncomplexed metal binding polypeptide and immunoassay complete the steps for this detection method.

Methods for detection that are based upon an immobilized metal binding polypeptide may utilize a radioactive version of the heavy metal or a similar tagged form thereof. Such tags include fluorescent, colorimetric and other spectrally active groups that can be coordinated or bonded to the heavy metal like the spacer arm. A preferred tag is a spacer arm containing a spectrally active group. First, the immobilized monoclonal antibody is saturated with the tagged heavy metal. After removal of the non-immobilized components, an aliquot of the unknown heavy metal is added. It displaces a portion of the bound, tagged heavy metal and measurement of that amount displaced will determine the concentration of unknown metal.

Methods for detection that are based upon an oscillating probe utilize either an immobilized spacer arm for the heavy metal or preferably immobilized metal binding polypeptide. This method measures the change in frequency of an oscillating surface as a function of the change in weight of that surface due to the binding of the non-immobilized heavy metal or metal binding

polypeptides are immobilized on the surface of a high frequency oscillating probe. The probe is placed into a medium containing an unknown quantity of heavy metal.

Binding of the heavy metal to the immobilized metal

- 5 binding polypeptide will change the oscillation frequency of the probe. Hence, the degree of change will indicate the level of heavy metal present.

When the heavy metal is present as a metal cation in an aqueous medium, an especially preferred method for

- 10 detection utilizes an oligopeptide having reactive group(s) capable of coordinating with the metal cation. The oligopeptide and the metal binding polypeptide specific for the metal cation unknown are added to the aqueous medium. The medium then is assayed for the
15 presence of metal binding polypeptide cation conjugate. The interaction of the metal binding polypeptide with the metal cation is independent of the order of addition of the reactants and is independent of the identity of the oligopeptide.

- 20 In an especially preferred version of this method, a fixed support is utilized. Here, either the oligopeptide or the metal binding polypeptide is immobilized on the fixed support. The method is then conducted as related above.

- 25 The invention, in addition, contemplates methods for heavy metal removal from, heavy metal neutralization within or heavy metal addition to biological or inanimate systems. For all methods, an effective amount of the metal binding polypeptide is combined in some
30 fashion with at least part of the system. Pursuant to the removal method, metal binding polypeptide-heavy metal conjugate is removed by separation means such as immunoprecipitation, immobilization, chromatography, filtration and the like. Pursuant to the neutralization
35 method, the metal binding polypeptide-heavy metal conjugate remains in the system until it is removed by non-specific means. Pursuant to the addition method,

the metal binding polypeptide-heavy metal conjugate also remains in the system and the heavy metal is actively incorporated or otherwise used therein.

When the system participating in the foregoing
5 methods is biological, the metal binding polypeptide may be combined with a pharmaceutically acceptable carrier. Preferably, the metal binding polypeptide will not of itself cause an undesirable immune response of the biological system. The biological systems contemplated
10 according to the invention include unicellular organisms, multicellular simple organisms, cellular component systems, tissue cultures, plants and animals, including mammals.

The present invention also contemplates methods for
15 removing heavy metallic cations or radioactive compounds from human fluids such as blood, serum or lymph by utilization of immobilized metal binding polypeptides. An extracorporeal shunt placed in the patient permits removal of the body fluid and its reintroduction.
20 Passing the body fluid extracorporeally through a bed of immobilized metal binding polypeptide accomplishes the desired removal.

The present invention also contemplates a kit for assaying the presence and quantity of heavy metal in a
25 biological or inanimate system. The kit includes aliquots of metal binding polypeptides in the appropriate buffer, as well as a fixed support for absorption of the heavy metal, washing solutions, reagents such as enzyme substrates, and metal binding
30 polypeptide specific antisera conjugated to a detectable substrate.

Brief Description of the Drawings

Figures 1A-1B depict the nucleotide and deduced
35 amino acid sequences for amino acids 1 through 113 of the heavy chain variable regions of monoclonal antibodies which immunoreact with a lead cation. The

numbering scheme is according to Kabat et al., Sequences of Proteins of Immunological Interest, vol. II. 5th edition, U.S. Department of Health and Human Services (1991) (hereinafter "Kabat"). Dashes indicate sequence identity with the 6B11 sequence; periods indicate gaps compared to the 1254 sequence.

Figure 2 depicts the nucleotide and deduced amino acid sequences for amino acids 5 through 108 of the light chain variable regions of monoclonal antibodies which immunoreact with a lead cation. The numbering scheme is according to Kabat. Dashes indicate sequence identity with the 6B11 sequence.

Figures 3A-3B depict the nucleotide and deduced amino acid sequences for amino acids 1 through 113 of the heavy chain variable regions of monoclonal antibodies which immunoreact with a lead cation. The numbering scheme is according to Kabat. Periods indicate gaps.

Figure 4 depicts the nucleotide and deduced amino acid sequences for amino acids 1 through 107 of the light chain variable regions of monoclonal antibodies which immunoreact with a lead cation. The numbering scheme is according to Kabat.

Figure 5 depicts the nucleotide and deduced amino acid sequences for amino acids 1 through 113 of the heavy chain variable regions of monoclonal antibody 2B4 which immunoreacts with a lead cation. The numbering scheme is according to Kabat.

Figure 6 depicts the nucleotide and deduced amino acid sequences for amino acids 1 through 113 of the heavy chain variable regions of monoclonal antibody 2E7 which immunoreacts with a lead cation. The numbering scheme is according to Kabat.

Figure 7 shows the sensitivity of a set of Group 1 monoclonal antibodies (standardized to 50 $\mu\text{g/mL}$ in PBS) to lead (as $\text{Pb}(\text{NO}_3)_2$). The indicated amounts of lead were added to a microtiter plate coated with an amino

acid polymer formed from glutamic acid, lysine, and tyrosine (hereinafter "EKY polymer") and analyzed by ELISA. The measured absorbances were corrected for the absorbance of an average of four control wells.

5 Figure 8 shows the sensitivity of a second set of Group 1 monoclonal antibodies (standardized to 50 $\mu\text{g/mL}$ in PBS) to lead (as $\text{Pb}(\text{NO}_3)_2$). The indicated amounts of lead were added to a microtiter plate coated with EKY polymer and analyzed by ELISA. The measured absorbances
10 were corrected for the absorbance of an average of four control wells.

 Figure 9 shows the sensitivity of a set Group 3 monoclonal antibodies (standardized to 50 $\mu\text{g/mL}$ in PBS) to lead (as $\text{Pb}(\text{NO}_3)_2$). The indicated amounts of lead
15 were added to a microtiter plate coated with EKY polymer and analyzed by ELISA. The measured absorbances were corrected for the absorbance of an average of four control wells.

 Figure 10 shows the sensitivity of a second set of
20 Group 3 monoclonal antibodies (standardized to 50 $\mu\text{g/mL}$ in PBS) to lead (as $\text{Pb}(\text{NO}_3)_2$). The indicated amounts of lead were added to a microtiter plate coated with EKY polymer and analyzed by ELISA. The measured absorbances were corrected for the absorbance of an average of four
25 control wells.

 Figure 11 shows the sensitivity of a third set of Group 3 lead cation monoclonal antibodies (standardized to 50 $\mu\text{g/mL}$ in PBS) to lead (as $\text{Pb}(\text{NO}_3)_2$). Monoclonal antibody 3A6, which is specific for the PR8 influenza
30 virus, was included as a control. The indicated amounts of lead were added to a microtiter plate coated with EKY polymer and analyzed by ELISA. The measured absorbances were corrected for the absorbance of an average of four control wells.

Detailed Description of the Invention

Metal binding polypeptides of the present invention are key to the development of methods for detecting, adding, neutralizing or removing minute quantities of heavy metals. Until the present invention, it was not possible to produce metal binding polypeptides which selectively bind with exposed heavy metal cations *per se*. The novel techniques for incorporating heavy metals into immunogen compounds and for administering these immunogen compounds to immune cell hosts allow production of the desired, immunospecific monoclonal antibodies according to the invention. These methods are believed to constitute an advancement in the understanding of immunology.

Although not intended as a limitation of the invention, it is now believed that mammalian immunogenic reactivity can be elicited by heavy metals. While they are smaller than the commonly recognized epitope size of approximately 20-25 angstroms, the heavy metals nevertheless can bind.

Notwithstanding these beliefs, the invention contemplates metal binding polypeptides which selectively bind with a heavy metal, e.g. monoclonal antibodies to heavy metals. Hybridomas for the monoclonal antibodies and immunogen compounds for carrying the heavy metals and inducing immunogenicity are also included in the present invention. The metal binding polypeptides may include a monoclonal antibody, a recombinantly produced Fab fragment or a fusion protein. The fusion protein includes the heavy chain variable region of a monoclonal antibody which is capable of immunoreacting with a heavy metal, such as a lead cation. The invention also provides methods for the detection, addition, neutralization or removal of heavy metals using the metal binding polypeptides.

Monoclonal Antibodies

The monoclonal antibodies of the invention are mammalian immunoglobulin proteins which have strong affinity constants for a specific heavy metal.

5 Preferably, the monoclonal antibodies are from the IgG, IgA, IgM and IgE classes of antibodies, and more preferably, from the IgA, and IgM classes of antibodies. The heavy metal monoclonal antibodies are typically characterized by selective immunoreactivity with a

10 particular heavy metal and a substantially lower immunoreactivity with other similarly structured heavy metals. Preferably, the monoclonal antibodies have an association constant for the selected heavy metal that is at least about 10,000 fold greater than the

15 association constant for any similarly structured heavy metal. With respect to heavy metal cations, the especially preferred IgM and IgA classes of monoclonal antibodies of the present invention exhibit discriminatory dissociation constants of about $10^{-6}M$ to

20 about $10^{-12}M$. Examples include monoclonal antibodies of the IgM class which are produced by hybridomas 6B11, 1254, 7D10, 4E8, 8E7, 14F11 (ATCC NO. HB 11330), 10G5 and 14G11 and have a dissociation constant for lead cation of less than about $10^{-9}M$ but do not bind cadmium,

25 copper, zinc, nickel and cobalt cations to any appreciable extent. Other examples include monoclonal antibodies of the IgM and IgA classes which are produced by hybridomas derived from the spleen cells of a mammal injected with a solution of antibodies capable of

30 immunoreacting with a lead cation. Suitable examples include monoclonal antibodies of the IgM class which are produced by hybridomas 13D10, 2E7, and 6F5. Monoclonal antibodies produced by hybridoma 11D11, 2B6, 13E8 and 8E7 are examples of antibodies of the IgA class which

35 are capable immunoreacting with a lead cation.

Immunogen Compounds

The immunogen compounds for generation of the specific immunogenicity of the monoclonal antibodies are based upon the hapten-carrier concept. The present invention, however, broadens this concept so that the hapten is coordinated at the end of a spacer arm covalently bonded to the carrier. The spacer arm is adapted so as to be semi-rigid and to hold the heavy metal in an exposed position relative to the carrier. This arrangement is also adapted to maintain the heavy metal in a substantially exposed and preferably, essentially completely exposed state. These factors combine substantially to avoid chelating, covering or inclusion of the heavy metal by the spacer arm and/or the carrier.

The spacer arm, as characterized above, may be an oligopeptide, an aliphatic compound, or an aliphatic fragment. In the latter two instances, the aliphatic compound or fragment may be covalently bonded to the carrier by means of a Schiff base reaction with an aldehyde group, an amide formation reaction with an amine or carboxylic acid group using a peptide activator such as carbodiimide, acid chloride and the like, an ester formation reaction with a hydroxyl or carboxylic acid group using a Schotten Bauman reaction, or azide or acid catalysis reaction, a sulfide reaction using a sulfide coupling agent, or other known coupling reactions for joining organic molecules to proteins. See for example Kabat, E.A., Structural Concepts In Immunology and Immunochemistry, 2nd Ed., Holt, Rinehart and Winston, New York, 1976 (a review text of such methods) and Jaime Eyzaguirre, Chemical Modification of Enzymes: Active Site Studies, John Wiley & Sons (1982), the disclosures of which are incorporated herein by reference. The oligopeptide, aliphatic compound or fragment will contain backbone groups which provide semi-rigidity to the spacer arm. Preferred groups for

developing this semi-rigidity include peptide bonds, olefin bonds, olefinic conjugated systems, ester groups and enone groups. Optionally, and especially where immunogenicity of the heavy metal appears difficult to generate, one or more aromatic rings can be incorporated into the spacer arm to stimulate the development of an immune response.

In general, the oligopeptide spacer arm has the following formula:

10 - X - (R) - Y

wherein X is a coupling group that will bond to the carrier, R is one or more amino acid residues and Y is the Lewis Acid or Base group(s) for heavy metal coordination.

15 In general, the aliphatic compound or fragment
spacer arm has the following formula:

- X - (Q) - Z

wherein X is a coupling group that will bond to the carrier, Q is a semirigid aliphatic moiety containing ester, amide, keto, olefin or aromatic groups and the like, and Z is a Lewis acid or Base group(s) for heavy metal coordination.

The oligopeptide or aliphatic compound is used as the spacer arm to coordinate a metal cation. In this instance, the pendent Lewis base groups will preferably be positioned at the spacer arm end remote from the carrier. These Lewis base groups function as the coordination site or sites for the metal cation. It is preferable that the deformability of the electron shells of the Lewis base groups and the metal cations be approximately similar. Accordingly, sulfur groups can serve as the Lewis base groups when the metal cations are transition metals or inner transition elements.

The carrier of the immunogen compound is a large
35 biopolymer that is known to participate in the
development of hapten antigenicity. Blood serum
proteins, amylopectins, polysaccharides, fetal serum

components, biologically acceptable natural and synthetic proteins and polyamides such as polyglycine can serve as the carriers. Preferred carriers include serum and tissue proteins. Examples are keyhole limpet
5 hemocyanin (KLH) and bovine serum albumin (BSA). Other examples include ovalbumin and chicken gamma globulin. These carriers have sites for coordinate bonding of the spacer arm. Such sites are preferably populated by amine groups, carboxylic acid groups, aldehyde groups
10 and/or alcohol groups.

Production of Hybridomas

The production of hybridomas according to the invention generally follows the Kohler, Milstein
15 technique cited supra. Many heavy metals, however, toxify the mammalian system being used as a source of immune cells. This effect makes it important to determine the highest allowable dose of heavy metal and/or immunogen compound that can be used over a
20 substantially long period of time without killing the host. Pursuant to the Kohler, Milstein technique, immunization of the mammalian host may be accomplished within this dose parameter by subcutaneous or intraperitoneal injection of the immunogen compound in
25 adjuvant. Administration is repeated periodically and preferably for at least four injections. Three days before the spleen is removed, a priming injection of immunogen compound is again administered.

After separation, the spleen cells are fused with
30 immortal mammal cells such as mouse myeloma cells using the techniques outlined by Kohler and Milstein. Polyethylene glycol (PEG) or electrical stimulation will initiate the fusions.

The fused cells are then cultured in cell wells
35 according to culture techniques known in the art. Cellular secretions in the culture medium are tested

after an appropriate time for the presence of the desired cellular products.

The induction of antibodies to heavy metals in a mammalian host may also be accomplished by subcutaneous or intraperitoneal injection of a lead cation monoclonal antibody solution in an adjuvant. These antibodies are typically derived from another animal of the same species. The spleen cells are then isolated and fused with immortal mammalian cells as described above. As before, the fused cells are cultured and the cellular secretions are examined for the presence of the desired antibodies ("Group 3 monoclonal antibodies").

The latter technique based on the induction of antibodies using a second lead cation antibody may be more efficient than the method based on the injection of a Pb(II)/glutathione/carrier immunogen compound into a mouse. Table 1 herein shows the relative success rate for induction of lead cation antibodies using the two techniques. The results shown in Table 1 demonstrate that the rate of generating lead cation monoclonal antibody producing hybridomas formation derived from injection of the 1254 mAb was greater than twenty fold more efficient than the method based on injection of the OVA/glutathione/Pb(II) immunogen compound. In fact, a single set of fusions of spleen cells from animals injected with the 1254 mAb produced more lead cation antibodies than the total number of lead cation antibodies produced by five sets of fusions of spleen cells induced with the immunogen compound.

30

Selection Technique

The selection technique for identifying the appropriate monoclonal antibody is an important aspect for determining the immunospecificity desired according to the invention. The selection techniques according to the invention call for determining the binding affinity of the hybridoma cellular products against the heavy

metal and against cross-reactive controls. In particular, hybridoma culture fluid is tested in screening assays against the heavy metal, the carrier, the carrier-spacer arm product and the immunogen

5 compound as well as optionally against the spacer arm-heavy metal coordinate. Screening assays can be performed by immunoenzymatic-assay, immunofluorescence, radioimmunoassay, immunoprecipitative assay or inhibition of biological activity.

10 The hybridoma cultures selected will exhibit strong binding characteristics to the heavy metal (and immunogen compound) and will not bind with the spacer arm-carrier product or with the carrier itself.

Following the identification of cell cultures
15 producing the desired monoclonal antibodies, subcloning to refine the selected culture can be performed. These techniques are known to those skilled in the art. See for example Goding, James Goding, Monoclonal Antibodies: Principles and Practice, 2nd Edition, Academic Press,
20 San Diego, CA 1986, the disclosure of which is incorporated herein by reference. Briefly, the appropriately selected cell culture is separated into one cell units which are then recultured. The subclone cultures are then again tested for specific
25 immunoreactivity, lack of cross-reactivity and the amount of monoclonal antibody secreted. Those subcultures exhibiting the highest amounts of secreted monoclonal antibody are chosen for subsequent pilot development.

30 Following the foregoing techniques, a number of hybridomas producing monoclonal antibodies to lead cations have been developed. Perpetual cell lines, designated 6B11, 1254 (8.15), 7D10, 4E8, 8E7, 17E5, 14F11, 10G5, 14G11 and 3H7, produce monoclonal
35 antibodies to lead cations. The group of cell lines were developed by inoculation of mice with an OVA/glutathione/Pb(II) conjugate. The sensitivity of

monoclonal antibodies produced by these hybridoma cell lines is shown in Figures 7 and 8. The sensitivity of mAb 3A6 (a monoclonal antibody specific for the PR8 influenza virus), which was included as a control, as anticipated, showed no sensitivity to Pb(II) (see Figure 8). Monoclonal antibody 4A10 was derived from the spleen cells of a mouse injected with a mercury cation. The monoclonal antibodies produced by hybridoma 4A10 cross react with Pb(II) cations as well as immunoreacting with a mercury cation.

Using similar fusion and selection techniques, a number of hybridomas producing monoclonal antibodies to lead cations were developed by inoculation of mice with different lead cation monoclonal antibodies ("Group 3 lead cation monoclonal antibodies"). Perpetual cell lines, designated 2B4, 2B6, 3B6, 13B7, 13B11, 16B11, 6C2, 14C6, 19C6, 11D11, 13D10, 2E7, 4E4, 12E5, 13E8, 18E7, 6F5, 1G4, 1G6, 6G2, and 13G9 were developed using this latter technique. The sensitivity of monoclonal antibodies produced by these hybridoma cell lines is shown in Figures 9-11. The set of Group 3 lead cation monoclonal antibodies exhibited lead sensitivity comparable to the "parent" Group 1 antibody, mAb 1254, and to other Group 1 lead cation monoclonal antibodies generated by injection of the OVA/glutathione/lead(II) immunogen compound.

The immunogenic host for these hybridomas was the BALB/c mouse and the fusion partner was chosen from the mouse myeloma cell lines P3X63-Ag8.653 or SP2/0. Immunizations to induce Group 1 lead cation antibodies were accomplished with the immunogen compound formed from ovalbumin, glutathione and lead(II) cation functioning as the heavy metal in complete Freund's adjuvant. Immunizations to induce Group 3 lead cation antibodies were accomplished with the lead cation monoclonal antibody designated 1254 ("mAb 1254") in an adjuvant. All of the cell lines mentioned above are

maintained in culture medium and in frozen medium at liquid nitrogen temperature.

PCR Amplification

5 PCR amplification of Fd and κ regions from the spleen messenger RNA (mRNA) of a mouse immunized with BSA-glutathione-lead cation may be performed as described by Sastry et al., Proc. Natl. Acad. Sci U.S.A., 86, 5728 (1989). The PCR amplification is
10 performed with cDNA obtained by the reverse transcription of the mRNA with a primer specific for amplification of heavy chain sequences or light chain sequences.

 The PCR amplification of mRNA isolated from spleen
15 cells or hybridomas with oligonucleotides that incorporate restriction sites into the ends of the amplified product may be used to clone and express heavy chain sequences (e.g., the amplification of the Fd fragment) and κ light chain sequences from mouse spleen
20 cells. The oligonucleotide primers, which are analogous to those that have been successfully used for amplification of V_H sequences (see Sastry et al., Proc. Natl. Acad. Sci U.S.A., 86, 5728 (1989)), may be used for these amplifications. Restriction endonuclease
25 recognition sequences are typically incorporated into these primers to allow for the cloning of the amplified fragment into a λ phage vector in a predetermined reading frame for expression.

30 Expression of Fab Fragments on Phage Coat

 Phage assembly proceeds via an extrusion-like process through the bacterial membrane. Filamentous phage M13 has a 406-residue minor phage coat protein (cpIII) which is expressed before extrusion and which
35 accumulates on the inner membrane facing into the periplasm of E. coli. The two functional properties of cpIII, infectivity and normal (nonpolyphage)

morphogenesis, have been assigned to roughly the first and second half of the gene. The N-terminal domain of cpIII binds to the F' pili, allowing for infection of E. coli, whereas the membrane-bound C-terminal domain,

- 5 P198-S406, serves the morphogenic role of capping the trailing end of the filament according to the vectorial polymerization model.

A phagemid vector may be constructed to fuse the antibody Fd chain with the C-terminal domain of cpIII
10 (see Barbas et al., Proc. Natl. Acad. Sci. USA, 88, 7978 (1991)). A flexible five-amino acid tether (GGGGS), which lacks an ordered secondary structure, may be juxtaposed between the expressed Fab and cpIII domains to minimize interaction. The phagemid vector may also
15 be constructed to include a nucleotide coding for the light chain of a Fab fragment. The cpIII/Fd fragment fusion protein and the light chain protein may be placed under control of separate lac promoter/operator sequences and directed to the periplasmic space by pelB
20 leader sequences for functional assembly on the membrane. Inclusion of the phage F1 intergenic region in the vector allows for packaging of single-stranded phagemid with the aid of helper phage. The use of helper phage superinfection may result in expression of
25 two forms of cpIII. Consequently, normal phage morphogenesis may be perturbed by competition between the cpIII/Fd fragment fusion protein and the native cpIII of the helper phage for incorporation into the virion. The resulting packaged phagemid may carry
30 native cpIII, which is necessary for infection, and the fusion protein including the Fab fragment, which may be displayed for interaction with an antigen and used for selection. Fusion at the C-terminal domain of cpIII is necessitated by the phagemid approach because fusion
35 with the infective N-terminal domain would render the host cell resistant to infection. The result is a phage displaying antibody combining sites ("Phabs"). The

antibody combining sites, such as Fab fragments, are displayed on the phage coat. This technique may be used to produce Phabs which display recombinantly produced Fab fragments (e.g., recombinantly produced Fab

5 fragments that immunoreact with a lead cation) on the phage coat of a filamentous phage such as M13.

A phagemid vector (pComb 3) which allows the display of antibody Fab fragments on the surface of filamentous phage, has been described (see Barbas et al., Proc. Natl. Acad. Sci. USA, 88, 7978 (1991)). *Xho*I and *Spe*I sites for cloning PCR-amplified heavy-chain Fd sequences are included in pComb 3. *Sac*I and *Xba*I sites are also provided for cloning PCR-amplified antibody light chains. These cloning sites are compatible with known mouse and human PCR primers (see, e.g., Huse et al., Science, 246, 1275-1281 (1989)). The nucleotide sequences of the pelB leader sequences are recruited from the λ HC2 and λ LC2 constructs described in Huse et al, ibid, with reading frames maintained. Digestion of pComb 3 encoding a selected Fab with *Spe*I and *Nhe*I permits the removal of the gene III fragment. Because *Spe*I and *Nhe*I produce compatible cohesive ends, the digested vector may also be religated to yield a phagemid that produces soluble Fab.

Phabs may be produced by overnight infection of phagemid containing cells (e.g., infected E. coli XL-1 Blue) yielding typical titers of 10^{11} cfu/mL. By using phagemids encoding different antibiotic resistances, ratios of clonally distinct phage may easily be determined by titering on selective plates. In single-pass enrichment experiments, clonally mixed phage may be incubated with an antigen-coated plate. Nonspecific phage will be removed by washing, and bound phage may then be eluted with acid and isolated.

Methods of Application

According to the invention, the metal binding polypeptide can be used to advantage for detection, neutralization, addition or removal of heavy metals from biological or inanimate systems. These methods apply to qualitative and quantitative analyses of minute concentrations of toxic metal cations, in aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. In each application, the presence of minute quantities of metallic cations could constitute deleterious contaminants. Their ready and early detection will avoid later production or regulatory setbacks.

Alternatively, the presence of minute quantities of heavy metals in certain instances may be desirable. For example, the presence of inorganic moieties in such mixtures as doping materials for semi-conductors and integrated circuits contributes to the properties of the product. Quality control of the presence and concentration of these heavy metals is essential for the functioning of the product. The detection methods of the invention enable ready and early measurement of the presence of such heavy metals and avoid later production or regulatory difficulties.

Heavy metals in biological or inanimate systems can also be removed by methods according to the invention. In the main, immobilization of the metal binding polypeptides on a solid support followed by its mixture with the materials of the biological or inanimate system will remove the heavy metals. In this instance, the immobilization of the monoclonal antibodies can be accomplished by techniques known to those of skill in

the art. See, for example, Affinity Chromatography, C.R. Fowe & P.D.G. Sean, John Wiley & Sons, London 1974, the disclosure of which is incorporated herein by reference. Removal is accomplished by passing a fluid
5 mixture of the system ingredients suspected of having the heavy metals over the immobilized metal binding polypeptides. Of course, the metal binding polypeptides are designed to be specific for the heavy metal sought to be removed.

10 An advantage of this method is the removal of undesirable heavy metals in the presence of similarly structured desirable metal species. For example, whole blood from a patient suffering from lead poisoning can be removed from the patient, optionally filtered to
15 return the cellular blood components to the patient, and the serum or blood passed over immobilized metal binding polypeptides specific for the lead. The purified serum or blood can then be returned to the patient. The lead will be removed but other blood serum components such as
20 zinc, calcium and the like will not.

Specific Applications

A particular application of the present invention contemplates a method for the production of monoclonal
25 antibodies specific for the lead cation or another toxic, heavy metal cation. In accordance with this method, the heavy metal cation in question is combined into an immunogen compound as described above and suspended in an aqueous medium. A preferred protein
30 carrier for the immunogen compound in this instance is an albumin, e.g., ovalbumin. Keyhole limpet hemocyanin is also a preferred carrier. The preferred spacer arm in this instance is an oligopeptide which has sulfonate or carboxylate groups capable of coordinating with the
35 heavy metal cation. The suspension of immunogen compound is used to immunize a host mammal such as a mouse following the techniques outlined above. The

laboratory strain of mouse designated BALB/c is particularly preferred.

Spleen cells of the immunized host are collected and converted into a suspension. These spleen cells are
5 fused with immortal cells as described above. Preferably, myeloma cells of the same animal species as the immunized host are used as the fusion partner. Typically, a cell fusion promoter such as polyethylene glycol is employed to cause formation of the hybridoma
10 cells. The hybridoma cells are diluted and cultured in a medium which does not allow for the growth of unfused cells.

The monoclonal antibodies produced and secreted by the hybridomas are thereafter assayed for the ability to
15 bind immunologically with the heavy metal cations used for immunization. The antibodies are further selected for lack of cross-reactivity with carrier, with carrier-spacer arm and with similar metallic cations. The preferred assay method in this context is an
20 enzyme-linked immunosorbent assay.

The resulting monoclonal antibodies are specific for heavy metal cations and exhibit strong immunoreaction to the heavy metal cations in the presence of spacer arm or the spacer arm-carrier
25 composition. Preferred monoclonal antibodies are selectively immunoreactive with lead cations.

The present invention also provides methods and kits for detecting the presence of a toxic heavy metal cation such as a lead cation. The methods and kits
30 include a metal binding polypeptide which selectively binds the heavy metal.

According to an embodiment of a method for detecting the presence of a specific heavy metal cation, an immobilized coordinating compound is combined with
35 the unknown mixture containing the toxic heavy metal cation. The heavy metal cation complexes with the coordinating compound and is immobilized thereto.

Removal of the non-immobilized components leaves the immobilized toxic heavy metal cation. Addition of the metal binding polypeptide specific for the targeted heavy metal cation forms an immobilized cation-metal binding polypeptide conjugate. Its presence and concentration can be assayed by an ELISA technique or other tagging or visualization technique known to those of skill in the art. In this process, of course, non-immobilized metal binding polypeptide is removed before the assay is conducted.

A kit for quantitatively measuring the presence of a heavy metal cation is a further aspect of the invention. The kit includes a metal binding polypeptide specific for the toxic metal cation in question. The metal binding polypeptide is preferably metered into several aliquots of varying, known concentration. The kit may also include the immobilized coordination compound, preferably, attached to a solid support such as the well of a microtiter plate or a chromatographic material. The kit also typically includes a visualization or tagging assay material for determination of the presence of the metal binding polypeptide-heavy metal cation conjugate. If desired, a meter or other device for detecting and signaling the level of visual or other reading from the assay may also be included.

The invention will be further characterized by the following examples. These examples are not meant to limit the scope of the invention which has been fully set forth in the foregoing description. Variation within the concepts of the invention are apparent to those skilled in the art.

Example 1
Lead Cation Monoclonal Antibodies

5 A. General Procedures

1. Generation of Hybridomas via Injection of
OVA/glutathione/Pb(II)

Hybridoma antibodies were produced from the spleen cells of BALB/c mouse that had received multiple
10 injections of lead(II) cations reacted with glutathione to produce a lead cation coordinate covalent compound, which was covalently bound to ovalbumin ("OVA/glutathione/Pb(II) antigen"). Glutathione is a
15 three amino acid residue peptide having one reactive sulfhydryl group which forms a coordinate bond with lead cations. The OVA/glutathione/ Pb(II) antigen in complete Freund's adjuvant was utilized to assist in the elicitation of an immune response in the host animal.

Of hybridomas isolated, some were determined to be
20 producing monoclonal antibody specific for glutathione. In addition, other hybridomas (6B11, 1254, 8E7, 10G5 and 14F11) were producing monoclonal antibodies that were strongly positive against glutathione-lead cation but negative against glutathione without lead cation. These
25 antibodies were subcloned by the process of limiting dilution for further characterization.

ELISA Analysis for Hybridoma Antibodies
Immunoreactive With Glutathione-Lead Cations

Microtiter plates (EIA/RIA grade) were treated with
30 BSA-glutathione, blocked with 1% polyvinyl alcohol in phosphate-buffered saline ("PBS") and used for the ELISA. One hundred microliters of lead nitrate (100 ppm in 100 mMolar Hepes pH 7.2) was added to the wells and incubated for 30 minutes. The plates were washed three
35 times with PBS containing 0.1% Triton X-100, and then the hybridoma culture supernatant was added for 30 minutes at room temperature. After washing the wells, goat anti-mouse antibodies conjugated to horseradish peroxidase were added. Following incubation for 30

minutes at room temperature, the plates were washed with PBS containing 0.1% Triton X-100, and 100 ul of ABTS peroxidase substrate was added to each well. After 15 min at room temperature the absorbance of each well was
5 read at 405 nanometers. In addition, the frozen hybridoma samples have been thawed from liquid nitrogen and assayed for persistence of antibody secretion after thawing.

10 2. Determination of Lead-Cation Specific Monoclonal Antibodies

The monoclonal antibodies may be assayed with various other metals for inhibition of binding of the monoclonal antibodies to lead cations. The cationic
15 metals assayed may include the ions of zinc, copper, cadmium, nickel, and arsenic. For instance, the inhibition of the binding of a monoclonal antibody which immunoreacts with immobilized glutathione-lead cations by various concentrations of divalent cations may be
20 examined. Metal ions at the indicated concentrations are incubated with culture fluid from the antibody in an ELISA plate. The absorbance at 405 nm may be determined for each sample, and the percent inhibition of each metal ion concentration determined by the formula given
25 above.

Further analysis of the monoclonal antibodies can establish if the antibodies are specific for the lead cations per se and that glutathione is not needed for the monoclonal antibodies to react with and bind to the
30 lead cations. The monoclonal antibodies may also be assayed against BSA-glutathione, BSA-glutathione-lead cations, and BSA-lead cations. Comparison with a negative control consisting of a monoclonal antibody specific for an unrelated antigen permits a
35 determination of whether the monoclonal antibodies bind to lead cation in the absence of glutathione.

PBS containing metal ions at the indicated concentrations may be added to microtiter wells to which

BSA-glutathione has been absorbed. After incubation at room temperature for 30 minutes, the plates are washed to remove unbound metals, and the plates are used for a standard ELISA to detect lead cations.

5

B. Particular Preparations

1. Linkage of Lead Cations to Protein Carriers

To prepare antigen for injection and immunoassay, 132 mg $\text{Pb}(\text{NO}_3)_2$ (400 μmol), 61 mg glutathione (200 μmol) and 54 mg NaCl were dissolved in 10 mL of water. After cold ethanol (30mL) was added, the resulting mixture was incubated for 30 minutes at 0°C. The reaction mixture was centrifuged at 10,000 g for 30 minutes, and the pellet was washed with 30 mL of cold ethanol. The pellet was dissolved in 200 mL of 40% dimethylformamide pH 4.8, containing 200 mg of 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide, and 1 g of either bovine serum albumin or OVA was added to the solution. The reaction mixture was stirred at room temperature overnight. The mixture was then centrifuged as above, resuspended in PBS, and dialyzed overnight at 4°C against 4 liters of PBS.

2. Immunization of BALB/c Mice

Multiple injections of the antigen prepared with 10 ug of protein per injection were made into BALB/c mice. Lead cation-glutathione-OVA emulsified in Freund's adjuvant was employed as the antigen. Complete adjuvant was used for the first two injections, while incomplete adjuvant was used for all subsequent injections. After the fourth injection, a drop of blood from the tail of each mouse was collected separately in 0.5 mL of PBS, and each sample was assayed by ELISA for the presence of antigen-specific antibody. The mice used for hybridoma production received an intraperitoneal injection consisting of 10 ug of antigen in PBS 3-4 days before cell fusion.

3. Hybridoma Production

The spleen was removed aseptically from a mouse, and the cells were isolated by placing the spleen in 5 mL of sterile PBS and teasing it with two sterile, 18-gauge hypodermic needles. The cell suspension was added to an empty sterile, conical, 15-mL centrifuge tube and tissue fragments were allowed to settle for 1-2 minutes. The cells still in suspension were placed in a tube similar to that above and centrifuged at 300 g for 10 minutes at room temperature. The cells were then washed 3 times by centrifugation in serum-free DMEM (Dulbecco's modified Eagle's medium). Spleen cells were co-pelleted with P3X63-Ag8.653 myeloma cells at a ratio of 4 spleen cells to 1 myeloma cell. The supernatant fluid was removed, and the pellet was suspended in 1 mL of 35% polyethylene glycol for 1 minute. The polyethylene glycol was gradually diluted by addition of increasing amounts of serum-free DMEM over a period of 15 minutes. The cells are then suspended in HAT medium (Monoclonal Antibodies, Kennett, McKean, Backitt, eds., Plenum Press (1981)) at a concentration of 2×10^5 myeloma cells per mL, and 100 μ L of the suspension were added to each well of 5 separate 96-well microtiter plates. The plates were incubated in 10% CO₂ at 37°C for one week. At that time, half of the culture fluid was withdrawn from each well and replaced by 2 drops of fresh HT medium (HAT medium without aminopterin), and the plates were incubated as above for another week. Then, approximately 100 μ L of culture fluid was taken from each well containing macroscopically visible cell growth, and the ELISA technique described infra was used for identification of those culture fluids containing lead cation-specific antibodies.

4. Enzyme-Linked Immunosorbent Assay (ELISA)

Polyvinyl chloride microtiter assay plates may be coated with antigen by addition of 50 μ l of lead

cation-glutathione-BSA or glutathione-BSA at a concentration of 5 ug/mL in PBS to each well of the plate. The plates are allowed to incubate at room temperature overnight to allow the antigen to dry on the plate. Next day the plates are blocked by addition of 200 μ L of 1% polyvinyl alcohol ("PVA") in PBS to each well; the addition of the PVA blocks the remaining protein-binding sites. The plates are incubated for 30 min at room temperature, then washed 3 times with ELISA wash (PBS with 0.1% of Triton X-100), 3 times with milliQ water. A 100 ppm solution of lead in 100mM Hepes at pH 7 is then added to the wells (100 μ L/well and allowed to incubate for 30-60 minutes at room temperature.

Fifty microliters of culture fluid to be assayed for the presence of antigen-specific antibody may be added to the appropriate well, and the plates are incubated at room temperature for 2 hours. The plates are again washed 3 times with ELISA wash, and 50 μ L of goat anti-mouse serum (Cooper Biomedical) diluted 1:1000 in 2% BSA in PBS are added to each well. After incubation and washing as above, 50 μ L of rabbit anti-goat serum conjugated to alkaline phosphatase (Sigma) diluted 1:1000 in 50 mM Tris-HCl, pH 8.0, containing 1 mM $MgCl_2$, 5% BSA and 0.04% NaN_3 , are added to each well. After being incubated and washed as above, 150 μ L of phosphatase substrate (0.4 mM dinitrophenyl phosphate in 1 M diethanolamine, pH 9.8, containing 25 mM $MgCl_2$) are added to each well.

The enzyme catalyzed conversion of dinitrophenol phosphate to dinitrophenol is typically allowed to proceed at room temperature for 30-60 minutes. The absorbance of each well at 405 nm (dinitrophenol) may be measured with a UV/Vis spectrometer.

The use of other enzymes as sensors is also possible provided that such enzymes can be linked to an appropriate antibody, and catalyze a reaction which

produces a color change. For example, beta galactosidase, urease, or horseradish peroxidase could be utilized in this context.

5. 5. Binding of Lead Cations to Immobilized Coordinating Spacer Arms

One hundred microliters of BSA-glutathione at a concentration of 5 ug/mL were added to the wells of a microtiter plate and allowed to dry overnight. The plates were then blocked with PVA as above. One hundred microliters of PBS containing a known concentration of lead cations were added to triplicate wells on the plate, which were then incubated at room temperature for 30 minutes. After this incubation period the plates are washed with ELISA wash to remove unbound metal ions and then used in the standard ELISA to measure reactivity with a lead cation-specific antibody.

6. 6. Assay of Lead Cation-Specific Antibodies Against BSA Glutathione, BSA Glutathione-Lead and BSA-Lead

Lead cation specific antibodies secreted from hybridomas such as 6B11, 1254, 8E7, 10G5 and 14F11 were assayed against BSA-glutathione and BSA-glutathione-lead cation. The results established that all five antibodies immunoreacted with BSA-glutathione that had bound lead, and did not immunoreact with BSA-glutathione lacking lead.

Example 2

30 Nucleotides Coding for Heavy Chain Fd Fragments and Light Chains from Lead Cation Monoclonal Antibodies

35 Synthesis of Nucleotides Encoding the Heavy and Light Chain Variable Regions of the Lead-Cation Antibodies

RNA was isolated from hybridoma cells with guanidine isothiocyanate (Evans et al., BioTechniques, 8, 357 (1990)), and enriched for poly(A) + RNA by passage over a poly(dT)-cellulose column (Aviv et al., Proc. Natl. Acad. Sci. USA, 69, 1408 (1972)). First-

strand cDNA synthesis was catalyzed by MuLv reverse transcriptase with a Promega RiboClone kit, according to the manufacturer's directions. The primers used for cDNA synthesis were complementary to the 5' end of the C_H1 domain of the heavy chain expressed by the hybridoma of interest, or to the 5' end of the C_κ domain. The following primers were used for cDNA synthesis:

KAPPA Primer - Light Chain

5¹-GAAGATCTAGACTTACTATGCAGCATCAGC-3¹ (SEQ ID
NO:41)

MU primer - Heavy Chain

5¹-AGGAGACTAGTGGTTACTAATTTGGGAAGGACTG-3¹ (SEQ ID
NO:42)

15 Amplification of Antibody Variable Regions by Polymerase Chain Reaction

The primer used for cDNA synthesis of the variable region of a particular antibody polypeptide chain was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer as described in Huse et al., Science, 246, 1275 (1989). The PCR was performed as described in Sastry et al., Proc. Natl. Acad. Sci. USA, 86, 5728 (1989).

25 Sequence Determination of Nucleotides Encoding the Heavy and Light Chain Variable Regions of the Lead Cation Antibodies

The PCR amplified nucleotide sequences encoding the heavy and light chain variable regions of the lead cation antibodies were cloned into Bluescript (Stratagene, La Jolla, CA). The sequences of these nucleotides were determined by the dideoxy chain termination method (Sanger et al., Proc. Natl. Acad. Sci. USA, 74, 5463 (1977)). The sequences of at least three PCR products for each heavy and light chain were determined to allow detection of incorporation errors by Taq polymerase. The nucleotide and deduced amino acid sequences of the heavy and light chain variable regions

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of the lead-specific antibodies are shown in Figures 1A-1B and 2.

Figures 1A-1B depict the nucleotide and deduced amino acid sequences for the heavy chain variable regions of a number of monoclonal antibodies that immunoreact with a lead cation. The following sequences are shown:

the heavy chain variable region nucleotide acid sequence and deduced amino acid sequence for monoclonal antibody 6B11 (SEQ ID NO:1);

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 1254 (SEQ ID NO:3);

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 8E7 (SEQ ID NO:5);

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 10G5 (SEQ ID NO:7); and

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 14F11 (SEQ ID NO: 9).

Figure 2 depicts the nucleotide and deduced amino acid sequences for the light chain variable regions of a number of monoclonal antibodies which immunoreact with a lead cation. The following sequences are shown:

the light chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 6B11 (SEQ ID NO: 11);

the light chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 1254 (SEQ ID NO:13); and

the light chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 14F11 (SEQ ID NO:15).

Figures 3A-3B depict the nucleotide and deduced amino acid sequences for the heavy chain variable

regions of a number of monoclonal antibodies that immunoreact with a lead cation. The following sequences are shown:

- 5 the heavy chain variable region nucleotide
acid sequence and deduced amino acid sequence for
monoclonal antibody 13D10 (SEQ ID NO:17);
- the heavy chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 11D11 (SEQ ID NO:19);
- 10 the heavy chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 14G11 (SEQ ID NO:21);
- the heavy chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 6F5 (SEQ ID NO:23);
- 15 the heavy chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 7D10 (SEQ ID NO:25); and
- the heavy chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 4E8 (SEQ ID NO:27).
- 20

Figure 4 depicts the nucleotide and deduced amino acid sequences for the light chain variable regions of a number of monoclonal antibodies which immunoreact with a lead cation. The following sequences are shown:

25

- the light chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 10G5 (SEQ ID NO:29);
- the light chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 2E7 (SEQ ID NO:31); and
- 30 the light chain variable region nucleotide
sequence and deduced amino acid sequence for
monoclonal antibody 7D10 (SEQ ID NO: 33).

35 Figure 5 depicts the nucleotide and deduced amino acid sequences for the heavy chain variable regions of

the monoclonal antibody 2B4 that immunoreacts with a lead cation. The following sequences are shown:

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 2B4 (SEQ ID NO:35).

Figure 6 depicts the nucleotide and deduced amino acid sequences for the heavy chain variable regions of the monoclonal antibody 2E7 that immunoreacts with a lead cation. The following sequences are shown:

the heavy chain variable region nucleotide sequence and deduced amino acid sequence for monoclonal antibody 2E7 (SEQ ID NO: 37).

As can be seen in the above-described amino acid sequences, (see, for example, figures 2 and 4) most of the light chains of the lead-reactive monoclonal antibodies are members of the $V_{\kappa}32$ light chain family, having a motif of four carboxylic acid-containing residues, e.g., glutamic acid and/or aspartic acid residues, in a stretch of five amino acids in the CDR1. Results of molecular modeling indicate that one or more of the carboxyl groups of these residues are positioned at the appropriate distance to form coordinate interactions with lead.

As described in the Examples, regardless of the specific antigen used for induction of lead-specific antibodies (e.g., anti-lead antibody or lead-containing complex), the majority of the resulting lead-reactive monoclonal antibodies contained light chains of the $V_{\kappa}32$ family.

Example 3

Expression of Fusion Proteins Including Heavy Chain Fd Fragments and Light Chains from Lead Cation Monoclonal Antibodies

1. Vector Construction

The pelB leader sequences and cloning sites for the heavy-chain fragment and light chain may be derived from phagemids excised from λ Hc2 and λ Lc2 vectors as

described in Huse, et al., Science, 246, 1275-1281 (1989). The sequences may be modified to remove a redundant *SacI* site from Hc2 phagemid and a *SpeI* site from the Lc2 phagemid. The combinatorial phagemid vector pComb is constructed from these two modified phagemids by restricting each with *ScaI* and *EcoRI* and combining them in a ligation reaction. Recombinants are screened for the presence of two *NotI* sites yielding the combinatorial vector pComb. The tether sequence GGGGS and gIII fragment (gene coding for coat protein III of filamentous phage M13 (see Barbas, et al., Proc. Natl. Acad. Sci. USA, 88, 7978 (1991)) from *SpeI* to *NheI* are the product of PCR of M13mpl8 (Yanisch-Perron, et al., Gene, 33, 103-119 (1985)) using the oligonucleotides 5'-GAGACGACTAGTGGTGGCGGTGGCTCTCCATTCGTTTGTGAATATCAA-3' (SEQ ID NO: 43) and 5'-TTACTAGCTAGCATAATAACGGAATACCCAAAAGAACTGG-3' (SEQ ID NO:44) as reported in Barbas, et al., Proc. Natl. Acad. Sci. USA, 88, 7978 (1991).

The *lacZ* promoter, operator, and Cap-binding site controlling light chain expression are the product of PCR with M13mpl8 using oligonucleotides 5'-TATGCTAGCTAGTAACACGACAGGTTTCCCGACTGG-3' (SEQ ID NO:45) and 5'-AGCTTTGAATTTCGTGAAATTGTTATCCGCT-3' (SEQ ID NO:46) as reported in Barbas et al., ibid. The PCR fragments encoding the gIII fragment and *lacZ* promoter are spliced by PCR overlap extension (see Horton et al., Gene, 77, 61-68 (1989)). The resulting product is digested with *SpeI* and *EcoRI* and ligated into the corresponding sites of pComb to yield pComb 3'. Finally, pComb 3' is digested with *XhoI* and *SpeI* and ligated with the corresponding 51-base-pair (bp) stuffer from pBluescript (see Short, et al., Nucleic Acids Res., 16, pp. 7583-7600 (1988)) (Stratagene) to yield pComb 3, an ampicillin-resistant phagemid.

2. Expression of Nucleotides on M13 Phage Coat Phage Production

A pComb 3 phagemid including a recombinantly produced Fab fragment that immunoreacts with a lead cation may be transformed into E. coli XL1-Blue cells. The transformed E. coli XL1-Blue cells may be grown in super broth medium (SB; 30 g of tryptone, 20 g of yeast extract, 10 g of Mops per liter, pH 7) at 37°C supplemented with tetracycline at 10 µg/ml and carbenicillin at 50 µg/mL or chloramphenicol at 30 µg/mL. Cultures are grown to an OD₆₀₀ of 0.4 and infected with VCSM13 helper phage (phage to cell ratio, 20:1) and grown an additional hour. After one hour kanamycin is added (70 µg/mL), and the culture is incubated overnight at 30°C. Phage may be isolated from liquid culture by polyethylene glycol 8000 and NaCl precipitation as described in Cwirla, et al., Proc. Natl. Acad. Sci. USA, 87, pp. 6378-6382 (1990). Phage pellets may be resuspended in phosphate-buffered saline (10 mM phosphate, pH 7.2, 150 mM NaCl) and stored at -20° C.

3. Single-Pass Enrichment Experiments

Phage expressing lead cation binding Fab fragments on their surface may be enriched by a modification of the panning procedure described by ParmLey, et al., Gene, 73, pp. 305-318 (1988). A single well of a microtiter plate (Costar 3690) is coated overnight at 4°C with 25 µL of BSA-glutathione-lead cation at 2 mg/mL in 0.1 M bicarbonate, pH 8.5. The well is washed once with water and blocked by filling the well with Blotto (1% (wt/vol) PVA in phosphate-buffered saline) and incubating the plate at 37°C for one hour. Blocking solution is shaken out, and 50 µl of clonally mixed phage (typically 10¹¹ colony-forming units (cfu)) is added, and the plate is incubated for an additional 2 hr at 37°C. Phage are removed, and the well is washed once with distilled water. The well is washed 10 times with TBS/Tween solution (50mM Tris-HCl, pH 7.5, 150 mM NaCl,

0.05% Tween 20) over a period of one hour at room temperature. The well is washed once more with distilled water, and adherent phage are eluted by adding 50 μ L of elution buffer (0.1 M HCl, adjusted to pH 2.2 with glycine), and incubation at room temperature for 10 min. The eluate is removed and neutralized with 3 μ L of 2 M Tris base. The initial phage input ratio may be determined by titering on selected plates. The final phage output ratio may be determined by infecting 1 mL of logarithmic phase XL1-Blue cells with the neutralized eluate for 15 min at room temperature and plating equal aliquots on selective carbenicillin and chloramphenicol plates.

4. Lead Cation-ELISA for Phabs

Equal plaque forming units from Phabs obtained from cultures of E. coli XL1-Blue cell may be transformed with a phagemid including a recombinantly produced Fab fragment that immunoreacts with a lead cation incubated at 37°C for two hours on BSA-Glutathione ELISA plates with or without lead nitrate. A rabbit anti-M13 antiserum is typically used as a second antibody followed by affinity-purified goat-antirabbit serum conjugated with peroxidase. 2,2'-Azino-Di-[3-ethylbenzthiazoline sulfonate] (ABTS) may be used as peroxidase substrate. The results are typically expressed as absorbance at 405 nanometers.

5. pComb3 Phagemid Expressing 1254 Light Chain

Using the methods described above, a pComb3 phagemid expressing only the light chain of monoclonal antibody 1254, without any accompanying heavy chain, was constructed. Two copies of the 1254 light chain sequence were cloned into the phagemid. Using the ELISA assay described above, the phagemid reacted with lead, demonstrating that the light chain of the antibodies is sufficient for lead binding.

Example 4Group 3 Lead Cation Monoclonal Antibodies1. Generation of Hybridomas via Injection of Lead Cation Monoclonal Antibody 1254

5 Group 3 antibodies were produced by injecting mice with the Group 1 lead cation monoclonal antibody, mAb 1254 (mAb 8.15). The mice were injected biweekly with 50 μ g of antibody emulsified in Freund's complete adjuvant and bled seven days after each injection. The
10 mice were bled by nicking the tail and collecting 50 μ l of blood, which was diluted to 500 μ l in phosphate buffered saline (PBS). The serum was tested using the same ELISA procedure as for screening the fusions (described below). The spleen cells of the mice were
15 then used for production of hybridoma monoclonal antibodies (mAb's) as described below.

Fusion Procedure for Hybridoma Production

 A mouse was sacrificed by cervical dislocation, and its spleen was removed aseptically. A single cell
20 suspension was prepared from the spleen, and the cells were washed three times in serum-free Dulbecco's modified Eagle's medium (DMEM) by centrifugation at 400x g for 10 minutes, with 10 ml of DMEM per wash. The number of viable spleen cells was determined by trypan
25 blue exclusion with a hemacytometer. The spleen cells were then mixed with SP2/0 myeloma cells at a ratio of 4 spleen cells:1 myeloma cell. The SP2/0 cells had previously been washed three times with serum-free DMEM as described above for the spleen cells.

30 The cell mixture was centrifuged as above, and the cell pellet was resuspended in 500 μ l of 50% polyethylene glycol (PEG 1500, Sigma Chemical Co., St. Louis, MO), which was added over a one-minute period. The cell suspension was stirred for an additional minute,
35 followed by addition of 10 ml of serum-free DMEM over the next two minutes. After stirring for an additional minute, the cells were centrifuged at 400x g for 10 minutes, and the pellet was resuspended in HAT medium to

a final concentration of 1×10^7 spleen cells/ml. Two hundred microliters of the cell suspension was added to each well of the appropriate number of 96-well microtiter plates, and the fusion was incubated at 37°C in an atmosphere of 10% CO₂, 90% air. All reagents and supplies used in this procedure were sterile and at room temperature.

Culture media

All culture media was filtered through a 0.2 μ m pore size filter (Nalgene).

A. Complete media

-Add the following to 500 milliliters of DMEM (Gibco):

- 10% of complement free (56 C for 1 hour) bovine calf serum (Hyclone)
- 45 millimolar of sodium pyruvate (Sigma)
- 200 millimolar of L-glutamine (Sigma)
- 0.1% of gentamicin (Gibco)

B. HT media

- Add the following to 500 milliliters of DMEM:
- 20% of complement free (56°C for 1 hour) fetal clone (Hyclone)
- 45 millimolar of sodium pyruvate (Sigma)
- 200 millimolar of L-glutamine (Sigma)
- 10 millimolar of hypoxanthine (Sigma)
- 1.5 millimolar thymidine (Sigma)
- 100 millimolar oxaloacetate (Sigma)
- 0.1% of gentamicin (Gibco)

C. HAT media

- Add the following to 500 milliliters of DMEM:
- 20% of complement free (56 C for 1 hour) fetal clone (Hyclone)
- 40 micromolar aminopterin (Sigma)
- 45 millimolar of sodium pyruvate (Sigma)
- 200 millimolar of L-glutamine (Sigma)
- 10 millimolar of hypoxanthine (Sigma)
- 1.5 millimolar thymidine (Sigma)

- 100 millimolar oxaloacetate (Sigma)
- 20 I.U./milliliter of bovine insulin (Sigma)
- 0.1% of gentamicin (Gibco)

5 2. Identification of Lead-Specific Antibodies by ELISA

 An amino acid polymer consisting of glutamic acid, lysine, and tyrosine at a ratio of 6:3:1 respectively ("EKY polymer"; Sigma Chemical Co.) was prepared as a 50 μ g/ml solution in PBS. One hundred microliters of the
10 EKY polymer solution was added to each well of a high-binding polystyrene plate (Corning Costar, Cambridge, MA). The plate was incubated at room temperature for thirty minutes, then rinsed three times with distilled water. One hundred microliters of 1% polyvinyl alcohol
15 (w/v) in PBS was added to each well, and the plate was incubated at room temperature for sixty minutes, after which it was rinsed as above.

 A Standard Reference Material (SRM) 3128 (National Institute of Standards and Technology, Gaithersburg, MD)
20 consisting of 10 mg/ml lead nitrate in 10% HNO₃ was diluted-tenfold in 1.0 M HEPES, pH 9.5. This solution was diluted to a final concentration of 100 μ g/ml in 0.1 M HEPES, pH 8.0. One hundred microliters of the resulting solution was added to each well of the plates
25 treated with the EKY polymer. The plates were incubated for 30 minutes and washed three times with distilled water before being used for ELISA.

 One hundred microliters of hybridoma culture fluid to be assayed for the presence of lead cation monoclonal
30 antibodies was added to the well of an antigen-coated microliter plate. The assay plate was incubated for 30 minutes at room temperature. The plate was then rinsed three times with ELISA wash (0.1% Triton X 100 in PBS) and three times with distilled water. One hundred
35 microliters of a 1:1000 dilution of goat anti-mouse IgA, IgG, IgM (Kirkegaard and Perry Laboratories, Gaithersburg, MD) conjugated to horseradish peroxidase

was added to each well. The plate was incubated at room temperature for thirty minutes, then rinsed as described above. After one hundred microliters of ABTS peroxidase substrate (Kirkegaard and Perry Laboratories) were added to each well and the plate was incubated at room temperature for fifteen minutes. The absorbance of each well at 405 nanometers was then measured on a Bio Tek Model EL-311 Plate Reader (Fisher, Pittsburgh, PA). The measured absorbances were compared to the absorbance of an average of four control wells. A hybridoma was considered positive if the absorbance of an assay well containing lead was twice that of a control well to which no lead had been added.

Positive hybridomas were subcloned by limiting dilution in 96-well microtiter plates in medium consisting of 50% HT medium and 50% complete DMEM conditioned by buffalo rat liver cells. Buffalo rat liver cells are known to secrete several somatomedin growth factors into the medium during growth. The somatomedin growth factors enhance the growth of cells in cloning situations.

3. Precipitation of Monoclonal Antibodies from Ascites Fluid

Ascites fluid was centrifuged at 300g for 10 minutes at 4°C to remove any particulate matter. The supernant fluid was decanted into a centrifuge tube and chilled in an ice bath for fifteen minutes. An ammonium sulfate solution was prepared by mixing 9 parts of a saturated solution of ammonium sulfate with 1 part distilled water. The resulting ammonium sulfate solution was added dropwise to an equal volume of ascites fluid while stirring gently. The mixture was stirred for an addition 4 hours at 4°C. The precipitate was pelleted by centrifugation at 3000 g for 30 minutes at 4°C. The pellet was resuspended in and dialyzed against PBS at 4°C.

The volume of the dialysate was measured, and two volumes of 60 millimolar sodium acetate, pH 4.0, was added to bring the final pH to 4.8. Caprylic acid (Sigma Chemical Co.) was added dropwise at a ratio of 0.4 milliliters per ten milliliters of the original volume of ascites fluid. The mixture was stirred at 4°C for four hours and centrifuged as above. The pellet was resuspended in PBS and dialyzed against PBS with 0.05% Triton X-100 for 24 hours then against PBS for 24 hours.

10

4. Measurement of the Sensitivity of the Lead-Specific Monoclonal Antibodies by ELISA

ELISA was carried out essentially as described in subsection 2 above except that the lead nitrate solution was diluted to final concentrations of 100, 50, 10, 5, or 1 µg/ml using 0.1 M HEPES, pH 8.0. One hundred microliters of each of these solutions was then added to the plate coated with the polyamino acid mixture. Caprylic acid-precipitated mAb was adjusted to a concentration of 50 µg/ml, and 100 µl was added to the appropriate wells of the microliter plate. The plate was incubated for 30 minutes at room temperature, and the ELISA was continued as described above.

25 All publications and patent applications in this specification are indicative of the level of ordinary skill in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated by reference.

30 The invention has been described with reference to various specific and preferred embodiments and techniques. However, it should be understood that many variations and modifications may be made while remaining within the spirit and scope of the invention.

SEQUENCE ID NO. DESIGNATIONS

SEQ ID #	ANTIBODY NAME	DESCRIPTION	SEQUENCE TYPE
1	6B11	Heavy Chain	Nucleic Acid
2	6B11	Heavy Chain	Amino Acid
3	1254	Heavy Chain	Nucleic Acid
4	1254	Heavy Chain	Amino Acid
5	8E7	Heavy Chain	Nucleic Acid
6	8E7	Heavy Chain	Amino Acid
7	10G5	Heavy Chain	Nucleic Acid
8	10G5	Heavy Chain	Amino Acid
9	14F11	Heavy Chain	Nucleic Acid
10	14F11	Heavy Chain	Amino Acid
11	6B11	Light Chain	Nucleic Acid
12	6B11	Light Chain	Amino Acid
13	1254	Light Chain	Nucleic Acid
14	1254	Light Chain	Amino Acid
15	14F11	Light Chain	Nucleic Acid
16	14F11	Light Chain	Amino Acid
17	13D10	Heavy Chain	Nucleic Acid
18	13D10	Heavy Chain	Amino Acid
19	11D11	Heavy Chain	Nucleic Acid
20	11D11	Heavy Chain	Amino Acid
21	14G11	Heavy Chain	Nucleic Acid
22	14G11	Heavy Chain	Amino Acid
23	6F5	Heavy Chain	Nucleic Acid
24	6F5	Heavy Chain	Amino Acid
25	7D10	Heavy Chain	Nucleic Acid
26	7D10	Heavy Chain	Amino Acid
27	4E8	Heavy Chain	Nucleic Acid
28	4E8	Heavy Chain	Amino Acid
29	10G5	Light Chain	Nucleic Acid
30	10G5	Light Chain	Amino Acid
31	2E7	Light Chain	Nucleic Acid
32	2E7	Light Chain	Amino Acid
33	7D10	Light Chain	Nucleic Acid
34	7D10	Light Chain	Amino Acid
35	2B4	Heavy Chain	Nucleic Acid
36	2B4	Heavy Chain	Amino Acid
37	2E7	Heavy Chain	Nucleic Acid
38	2E7	Heavy Chain	Amino Acid
39	6F5	Light Chain	Nucleic Acid
40	6F5	Light Chain	Amino Acid
41	KAPPA Primer	Light Chain	Nucleic Acid
42	MU Primer	Heavy Chain	Nucleic Acid
43	n.a. primer		Nucleic Acid
44	n.a. primer		Nucleic Acid
45	n.a. primer	Light Chain	Nucleic Acid
46	n.a. primer	Light Chain	Nucleic Acid

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Table 1. Comparison of the Fusion Efficiencies in Group 1 versus Group 3 Fusions

<u>Group/fusion</u>	<u># Cells Fused</u>	<u># Positives</u>	<u># Positives/10⁷ cells fused</u>
1A	19.0 x 10 ⁷	5	0.26
1B	18.6 x 10 ⁷	1	0.05
1C	11.2 x 10 ⁷	1	0.09
1D	18.7 x 10 ⁷	1	0.05
1E	12.2 x 10 ⁷	1	0.08
Average	15.9 x 10 ⁷	2.8	0.18
3	17.7 x 10 ⁷	66	3.73
Control	14.5 x 10 ⁷	0	0.0

Table 2. Class Analysis of Group 1 Lead Antibodies

#	Group	Hybridoma	Heavy Chain	Light Chain
1	1	8.15	μ	κ
2	1	4A10	μ	κ
3	1	3H7	μ	κ
4	1	4E8	μ	κ
5	1	6B11	μ	κ
6	1	7D10	μ	κ
7	1	8E7	μ	κ
8	1	10G5	μ	κ
9	1	14F11	μ	κ
10	1	14G11	μ	κ
11	1	17E5	μ	κ

Table 3. Class Analysis of Group 3 Lead-Specific Antibodies

#	Group	Clone	Heavy Chain	Light Chain
1	3	1G4	μ	κ
2	3	1G6	μ	κ
3	3	2B4	μ	κ
4	3	2B6	α	κ
5	3	2E7	μ	μ
6	3	3B6	μ	κ
7	3	4E4	μ	κ
8	3	6C2	μ	κ
9	3	6F5	μ	κ
10	3	6G2	μ	κ
11	3	11D11	α	λ
12	3	12E5	μ	κ
13	3	13B7	μ	κ
14	3	13B11	μ	κ
15	3	13D10	μ	κ
16	3	13E8	α	κ
17	3	13G9	μ	κ
18	3	14C6	μ	κ
19	3	16B11	μ	κ

Table 3. Class Analysis of Group 3 Lead-Specific Antibodies (continued)

20	3	18E7	α	κ
21	3	19C6	μ	κ

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:

- (A) NAME: BioNebraska, Inc.
- (B) STREET: 3820 Northwest 46th Street
- (C) CITY: Lincoln
- (D) STATE: Nebraska
- (E) COUNTRY: United States of America
- (F) POSTAL CODE (ZIP): 68524

(ii) TITLE OF THE INVENTION: LEAD BINDING POLYPEPTIDES AND NUCLEOTIDES CODING THEREFORE

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
- (B) STREET: 3100 Norwest Center, 90 South Seventh St
- (C) CITY: Minneapolis
- (D) STATE: MN
- (E) COUNTRY: USA
- (F) ZIP: 55402

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US96/09258
- (B) FILING DATE: 05-JUN-1996
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/541,373
- (B) FILING DATE: 10-OCT-1995

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/462,798
- (B) FILING DATE: 05-JUN-1995

(ix) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kettelberger, Denise M
- (B) REGISTRATION NUMBER: 33,924
- (C) REFERENCE/DOCKET NUMBER: 8648.49WOI2

(x) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 612/371-5268
- (B) TELEFAX: 612/332-9081
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...354

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAG GTT CAG CTG CAG CAG TCT GGA CCT GAG CTG GTG AGG CCT GGA CCT	48
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Pro	
1 5 10 15	
TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC TCC TTC ACC AGC TAC	96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr	
20 25 30	
TGG ATG AAC TGG GTG AAG CAG AGG CCT GGA CGA GGA CTT GAG TGG ATT	144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile	
35 40 45	
GGC ATG ATT CAT CCT TCC GAT AGT GAA ACT AGG TTA AAT CAG AAG TTC	192
Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe	
50 55 60	
AAG GAC AAG GCC ACA TTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC	240
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
ATG CAA CTC AGC AGC CCG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT	288
Met Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
GCA AGA AGG GGT AAC TCC GCC TGG TTT GCT TAC TGG GGC CAA GGG ACT	336
Ala Arg Arg Gly Asn Ser Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr	
100 105 110	
CTG GTC ACT GTC TCT GCA	354
Leu Val Thr Val Ser Ala	
115	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Pro
 1           5           10           15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
      20           25           30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
      35           40           45
Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
      50           55           60
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
      65           70           75           80
Met Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
      85           90           95
Ala Arg Arg Gly Asn Ser Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
      100          105          110
Leu Val Thr Val Ser Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...366

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAG GTC CAG CTG CAG CAG TCT GGA GCT GGG CTG GTG AAA CCC GGG GCA	48
Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Val Lys Pro Gly Ala	
1 5 10 15	
TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACT GAG TAT	96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr	
20 25 30	
ATT ATA CAC TGG GTA AAG CAG AGG TCT GGA CAG GGT CTT GAG TGG ATT	144
Ile Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
GGG TGG TTT TAC CCT GGA AGT GGT AGT ATA AAG TAC AAT GAG AAA TTC	192
Gly Trp Phe Tyr Pro Gly Ser Gly Ser Ile Lys Tyr Asn Glu Lys Phe	
50 55 60	
AAG GAC AAG GCC ACA TTG ACT GCG GAC AAA TCC TCC AGC ACA GTC TAT	240
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr	
65 70 75 80	
ATG GAG CTT AGT AGA TTG ACA TCT GAA GAC TCT GCG GTC TAT TTC TGT	288
Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	
85 90 95	
GCA AGA CAC GAA GGG TAT GGT AAC TAC GTG GCC TGG TTT GCT TAC TGG	336
Ala Arg His Glu Gly Tyr Gly Asn Tyr Val Ala Trp Phe Ala Tyr Trp	
100 105 110	
GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA	366
Gly Gln Gly Thr Leu Val Thr Val Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Val Lys Pro Gly Ala
 1           5           10           15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
      20           25           30
Ile Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile
      35           40           45
Gly Trp Phe Tyr Pro Gly Ser Gly Ser Ile Lys Tyr Asn Glu Lys Phe
      50           55           60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
      65           70           75           80
Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
      85           90           95
Ala Arg His Glu Gly Tyr Gly Asn Tyr Val Ala Trp Phe Ala Tyr Trp
      100          105          110
Gly Gln Gly Thr Leu Val Thr Val Ser Ala
      115          120

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...357
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAG GTC CAG CTG CAG CAG TCT GGG GCT GAG CTT GTG AAG CCT GGG GCT	48
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala	
1 5 10 15	
CCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACC AGC TAC	96
Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	
20 25 30	
TGG ATG AAC TGG GTG AAG CAG AGG CCT GGA CGA GGC CTC GAG TGG ATT	144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile	
35 40 45	
GGA AGG ATT GAT CCT TCC GAT AGT GAA ACT CAC TAC AAT CAA AAG TTC	192
Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe	
50 55 60	
AAG GAC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC	240
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
ATC CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT	288
Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
GCA AGA CAT CAC TAC GGC TAC TAT GCT ATG GAC TAC TGG GGT CAA GGA	336
Ala Arg His His Tyr Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly	
100 105 110	
ACC TCA GTC ACC GTC TCC TCA	357
Thr Ser Val Thr Val Ser Ser	
115	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala	
1 5 10 15	
Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	
20 25 30	
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile	
35 40 45	
Gly Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe	
50 55 60	
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg His His Tyr Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly	
100 105 110	
Thr Ser Val Thr Val Ser Ser	
115	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...354

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAG GTC CAG CTG CAG CAG TCT GGG GCT GAG CTG GTG AGG CCT GGA GCT	48
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala	
1 5 10 15	
TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC TCC TTC ACC AGC TAC	96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr	
20 25 30	
TGG ATG AAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT GAG TGG ATT	144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
GGC ATG ATT CAT CCT TCC GAT AGT GAA ACT AGG TTA AAT CAG AAG TTC	192
Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe	
50 55 60	
AAG GAC AAG GCC ACA TTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC	240
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
ATG CAA CTC AGC AGC CCG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT	288
Met Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
GCA AGA AGG AGG GAT TAC GAC CCG TTT GCT TAC TGG GGC CAA GGG ACT	336
Ala Arg Arg Arg Asp Tyr Asp Pro Phe Ala Tyr Trp Gly Gln Gly Thr	
100 105 110	
CTG GTC ACT GTC TCT GCA	354
Leu Val Thr Val Ser Ala	
115	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	1	5	10	15
Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr	20	25	30	
Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Met	Ile	His	Pro	Ser	Asp	Ser	Glu	Thr	Arg	Leu	Asn	Gln	Lys	Phe	50	55	60	
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	65	70	75	80
Met	Gln	Leu	Ser	Ser	Pro	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Arg	Arg	Asp	Tyr	Asp	Pro	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	100	105	110	
Leu	Val	Thr	Val	Ser	Ala											115			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...357

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAG GTC CAG CTG CAG CAG TCT GGA GCT GAG CTG GTA AGG CCT GGG ACT	48
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr	
1 5 10 15	
TCA GTG AAG GTG TCC TGC AAG GCT TCT GGA TAC GCC TTC ACT AAT TAC	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr	
20 25 30	
TTG ATA GAG TGG GTA AAG CAG AGG CCT GGA CAG GGC CTT GAG TGG ATT	144
Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
GGA GTG ATT AAT CCT GGA AGT GGT GGT ACT AAC TAC AAT GAG AAG TTC	192
Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe	
50 55 60	
AAG GGC AAG GCA ACA CTG ACT GCA GAC AAA TCC TCC AGC ACT GCC TAC	240
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
ATG CAG CTC AGC AGC CTG ACA TCT GAT GAC TCT GCG GTC TAT TTC TGT	288
Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys	
85 90 95	
GCA AGA AGC GGC TAC GGC CAC TGG TAC TTC GAT GTC TGG GGC GCA GGG	336
Ala Arg Ser Gly Tyr Gly His Trp Tyr Phe Asp Val Trp Gly Ala Gly	
100 105 110	
ACC ACG GTC ACC GTC TCC TCA	357
Thr Thr Val Thr Val Ser Ser	
115	

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
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[illegible]

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...312

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACC CAG TCT CCA TCA TCC CTG TCC ATG GCT ATA GGA GAA AAA GTC ACC	48
Thr Gln Ser Pro Ser Ser Leu Ser Met Ala Ile Gly Glu Lys Val Thr	
1 5 10 15	
ATC AGA TGC ATA ACC AGC ACT GAT ATT GAT GAT GAT ATG AAC TGG TAC	96
Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr	
20 25 30	
CAG CAG AAG CCA GGG GAA CCT CCT AAA CTC CTT ATT TCA GAA GGC AAT	144
Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile Ser Glu Gly Asn	
35 40 45	
ACT CTT CGT CCT GGA GTC CCA TCC CGA TTC TCC AGC AGT GGC TAT GGT	192
Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Tyr Gly	
50 55 60	
ACA GAT TTT GTT TTT ACA ATT GAA AAC ATG CTC TCA GAA GAT GTT GCA	240
Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser Glu Asp Val Ala	
65 70 75 80	
GAT TAC TAC TGT TTG CAA AGT GAT AAC TTG CCT CTC ACG TTC GGA GGG	288
Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu Thr Phe Gly Gly	
85 90 95	
GGG ACC AAG CTG GAA ATA AAA CGG	312
Gly Thr Lys Leu Glu Ile Lys Arg	
100	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Met	Ala	Ile	Gly	Glu	Lys	Val	Thr
1				5					10					15	
Ile	Arg	Cys	Ile	Thr	Ser	Thr	Asp	Ile	Asp	Asp	Asp	Met	Asn	Trp	Tyr
			20					25					30		
Gln	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile	Ser	Glu	Gly	Asn
		35						40				45			
Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser	Ser	Gly	Tyr	Gly
	50					55					60				
Thr	Asp	Phe	Val	Phe	Thr	Ile	Glu	Asn	Met	Leu	Ser	Glu	Asp	Val	Ala
65					70					75				80	
Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Leu	Pro	Leu	Thr	Phe	Gly	Gly
			85					90						95	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg								
			100												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...312

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACC CAG TCT CCA TCA TCC CTG TCC ATG GCT ATA GGA GAA AAA GTC ACC	48
Thr Gln Ser Pro Ser Ser Leu Ser Met Ala Ile Gly Glu Lys Val Thr	
1 5 10 15	
ATC AGA TGC ATA ACC AGC ACT GAT ATT GAT GAT GAT ATG AAC TGG TAC	96
Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr	
20 25 30	
CAG CAG AAG CCA GGG GAA CCT CCT AAA CTC CTT ATT TCA GAA GGC AAT	144
Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile Ser Glu Gly Asn	
35 40 45	
ACT CTT CGT CCT GGA GTC CCA TCC CGA TTC TCC AGC AGT GGC TAT GGT	192
Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Tyr Gly	
50 55 60	
ACA GAT TTT GTT TTT ACA ATT GAA AAC ATG CTC TCA GAA GAT GTT GCA	240
Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser Glu Asp Val Ala	
65 70 75 80	
GAT TAC TAC TGT TTG CAA AGT GAT AAC TTG CCT CTC ACG TTC GGT GCT	288
Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu Thr Phe Gly Ala	
85 90 95	
GGG ACC AAG CTG GAG CTG AAA GGG	312
Gly Thr Lys Leu Glu Leu Lys Gly	
100	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Thr Gln Ser Pro Ser Ser Leu Ser Met Ala Ile Gly Glu Lys Val Thr
 1          5          10          15
Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr
          20          25          30
Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile Ser Glu Gly Asn
          35          40          45
Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Tyr Gly
          50          55          60
Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser Glu Asp Val Ala
          65          70          75          80
Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu Thr Phe Gly Ala
          85          90          95
Gly Thr Lys Leu Glu Leu Lys Gly
          100

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...312

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACC CAG TCT CCA GCA TCC CTG TCC ATG GCT ATA GGA GAA AAA GTC ACC	48
Thr Gln Ser Pro Ala Ser Leu Ser Met Ala Ile Gly Glu Lys Val Thr	
1 5 10 15	
ATC AGA TGC ATA ACC AGC ACT GAT ATT GAT GAT GAT ATG AAC TGG TAC	96
Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr	
20 25 30	
CAG CAG AAG CCA GGG GAA CCT CCT AAG CTC CTT ATT TCA GAA GGC AAT	144
Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile Ser Glu Gly Asn	
35 40 45	
ACT CTT CGT CCT GGA GTC CCA TCC CGA TTC TCC AGC AGT GGC TAT GGT	192
Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Tyr Gly	
50 55 60	
ACA GAT TTT GTT TTT ACA ATT GAA AAC ATG CTC TCA GAA GAT GTT GCA	240
Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser Glu Asp Val Ala	
65 70 75 80	
GAT TAC TAC TGT TTG CAA AGT GAT AAC TTG CCG CTC ACG TTC GGT GCT	288
Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu Thr Phe Gly Ala	
85 90 95	
GGG ACC AAG CTG GAG CTG AAA CGG	312
Gly Thr Lys Leu Glu Leu Lys Arg	
100	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Thr Gln Ser Pro Ala Ser Leu Ser Met Ala Ile Gly Glu Lys Val Thr
 1          5          10          15
Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr
          20          25          30
Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile Ser Glu Gly Asn
          35          40          45
Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Tyr Gly
          50          55          60
Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser Glu Asp Val Ala
          65          70          75          80
Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu Thr Phe Gly Ala
          85          90          95
Gly Thr Lys Leu Glu Leu Lys Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...357

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAT GTG CAG CTT CAG GAG TCG GGA CCT GGC CTG GTG AAA CCT TCT CAG	48
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln	
1 5 10 15	
TCT CTG TCC CTC ACC TGC ACT GTC ACT GGC TAC TCA ATC ACC AGT GAT	96
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp	
20 25 30	
TAT GCC TGG AAC TGG ATC CGG CAG TTT CCA GGA AAC AAA CTG GAG TGG	144
Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp	
35 40 45	
ATG GGC TAC ATA AGC TAC AGT GGT AGC ACT AGC TAC AAC CCA TCT CTC	192
Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu	
50 55 60	
AAA AGT CGA ATC TCT ATC ACT CGA GAC ACA TCC AAG AAC CAG TTC TTC	240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe	
65 70 75 80	
CTG CAG TTG AAT TCT GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT	288
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys	
85 90 95	
GCA AGA TGT GGT AAC TAC CCG TGG TAC TTT GAC TAC TGG GGC CAA GGC	336
Ala Arg Cys Gly Asn Tyr Pro Trp Tyr Phe Asp Tyr Trp Gly Gln Gly	
100 105 110	
ACC ACT CTC ACA GTC TCC TCA	357
Thr Thr Leu Thr Val Ser Ser	
115	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1          5          10          15
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20          25          30
Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35          40          45
Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu
 50          55          60
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65          70          75          80
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
 85          90          95
Ala Arg Cys Gly Asn Tyr Pro Trp Tyr Phe Asp Tyr Trp Gly Gln Gly
100          105          110
Thr Thr Leu Thr Val Ser Ser
115

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...357

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAG GTT CAG CTG CAG CAG TCT GGA GTT GAG CTG ATG AAG CCT GGG GCC	48
Gln Val Gln Leu Gln Gln Ser Gly Val Glu Leu Met Lys Pro Gly Ala	
1 5 10 15	
TCA GTG AAG ATA TCC TGC AAG GCT ACT GGC TAC ACA TTC AGT AGC TAC	96
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr	
20 25 30	
TGG ATA GAG TGG GTA AAG CAG AGG CCT GGA CAT GGC CTT GAG TGG ATT	144
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile	
35 40 45	
GGA GAG ATT TTA CCT GGA AGT GGT AGT ACT AAC TAC AAT GAG AAG TTC	192
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe	
50 55 60	
AAG GGC AAG GCC ACA TTC ACT GCA GAT ACA TCC TCC AAC ACA GCC TAC	240
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr	
65 70 75 80	
ATG CAA GTC AGC AGC CTG ACA TCT GAG GAC TCT GCC GTC TAT TAC TGT	288
Met Gln Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
GCA AGG ATC TAC TAT GGT CAC TTG TGG TTT GCT TAC TGG GGC CAA GGG	336
Ala Arg Ile Tyr Tyr Gly His Leu Trp Phe Ala Tyr Trp Gly Gln Gly	
100 105 110	
ACT CTG GTC ACT GTC TCT GCA	357
Thr Leu Val Thr Val Ser Ala	
115	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Gln Val Gln Leu Gln Gln Ser Gly Val Glu Leu Met Lys Pro Gly Ala
 1           5           10           15
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
 20           25           30
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
 35           40           45
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
 50           55           60
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 65           70           75           80
Met Gln Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85           90           95
Ala Arg Ile Tyr Tyr Gly His Leu Trp Phe Ala Tyr Trp Gly Gln Gly
100           105           110
Thr Leu Val Thr Val Ser Ala
115

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...354

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAG	GTC	CAG	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AGG	TCA	GGG	GCC	48
Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Ser	Gly	Ala	
1				5					10					15		
TCA	GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	TAC	96
Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Tyr	
			20					25					30			
TAT	ATG	CAC	TGG	GTG	AAG	CAG	AGG	CCT	GAA	CAG	GGC	CTG	GAG	TGG	ATT	144
Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
GGA	TGG	ATT	GAT	CCT	GAG	AAT	GGT	GAT	ACT	GAA	TAT	GAC	CCG	AAG	TTC	192
Gly	Trp	Ile	Asp	Pro	Glu	Asn	Gly	Asp	Thr	Glu	Tyr	Asp	Pro	Lys	Phe	
		50				55				60						
CAG	GGC	AAG	GCC	ACT	ATG	ACT	GCA	GAC	ACA	TCC	TCC	AAT	ATA	GCC	TAC	240
Gln	Gly	Lys	Ala	Thr	Met	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Ile	Ala	Tyr	
65					70				75					80		
CTG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAT	ACT	GCC	GTC	TAT	TAC	TGT	288
Leu	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85				90						95		
AAT	CCC	TAT	GGT	TAC	GAC	GAT	GCT	ATG	GAC	TAC	TGG	GGA	CAA	GGA	ACC	336
Asn	Pro	Tyr	Gly	Tyr	Asp	Asp	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	
			100				105						110			
TCA	GTC	ACC	GTC	TCC	TCA											354
Ser	Val	Thr	Val	Ser	Ser											
																115

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Ser	Gly	Ala	1	5	10	15
Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Tyr	20	25	30	
Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Trp	Ile	Asp	Pro	Glu	Asn	Gly	Asp	Thr	Glu	Tyr	Asp	Pro	Lys	Phe	50	55	60	
Gln	Gly	Lys	Ala	Thr	Met	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Ile	Ala	Tyr	65	70	75	80
Leu	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Asn	Pro	Tyr	Gly	Tyr	Asp	Asp	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	100	105	110	
Ser	Val	Thr	Val	Ser	Ser											115			

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...330

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAG TCT GGT GGA GGA TTG GTG CAG CCT AAA GGG TCA TTG AAA CTC TCA	48
Glu Ser Gly Gly Leu Val Gln Pro Lys Gly Ser Leu Lys Leu Ser	
1 5 10 15	
TGT GCA GCC TCT GGA TTC ACC TTC AAT ACC TAC GCC ATG AAC TGG GTC	96
Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn Trp Val	
20 25 30	
CGC CAG GCC CCA GGA AAG GGT TTG GAA TGG GTT GCT CGC ATA AGA AGT	144
Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser	
35 40 45	
AAA AGT AAT AAT TAT GCA ACA TAT TAT GCC GAT TCA GTG AAA GAC AGG	192
Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg	
50 55 60	
TTC ACC ATC TCC AGA GAT GAT TCA CAA AGC ATG CTC TAT CTG CAA ATG	240
Phe Thr Ile Ser Arg Asp Asp Ser Gln Ser Met Leu Tyr Leu Gln Met	
65 70 75 80	
AAC AAC TTG AAA ACT GAG GAC ACA GCC ATG TAT TAC TGT GTG AGA CGG	288
Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr Tyr Cys Val Arg Arg	
85 90 95	
TTT GCT TAC TGG GCC CAA GGG ACT CTG GTC ACT GTC TCT GCA	330
Phe Ala Tyr Trp Ala Gln Gly Thr Leu Val Thr Val Ser Ala	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Lys	Gly	Ser	Leu	Lys	Leu	Ser	1	5	10	15
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Thr	Tyr	Ala	Met	Asn	Trp	Val	20	25	30	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile	Arg	Ser	35	40	45	
Lys	Ser	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Asp	Arg	50	55	60	
Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Gln	Ser	Met	Leu	Tyr	Leu	Gln	Met	65	70	75	80
Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Val	Arg	Arg	85	90	95	
Phe	Ala	Tyr	Trp	Ala	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala			100	105	110	

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...357

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAA GTT AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA	48
Glu Val Lys Leu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ACT TTC AGT AAC TAC	96
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr	
20 25 30	
TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT	144
Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val	
35 40 45	
GCT GAA GTT AGA TTG AAA TCT AAT TAT GCA ACA CAT TAT GCG GAG TCT	192
Ala Glu Val Arg Leu Lys Ser Asn Tyr Ala Thr His Tyr Ala Glu Ser	
50 55 60	
GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT AGT GTC	240
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val	
65 70 75 80	
TAC CTG CAA ATG AAC AAC TTA AGA GCT GAA GAC ACT GGA ATT TAT TAC	288
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr	
85 90 95	
TGT ACC CGT TAC GGT AGA GAG GGG GGG GTT GCT TAC TGG GGG CAA GGG	336
Cys Thr Arg Tyr Gly Arg Glu Gly Gly Val Ala Tyr Trp Gly Gln Gly	
100 105 110	
ACT CTG GTC ACT GTC TCT GCA	357
Thr Leu Val Thr Val Ser Ala	
115	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20          25          30
Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35          40          45
Ala Glu Val Arg Leu Lys Ser Asn Tyr Ala Thr His Tyr Ala Glu Ser
 50          55          60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val
 65          70          75          80
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr
 85          90          95
Cys Thr Arg Tyr Gly Arg Glu Gly Gly Val Ala Tyr Trp Gly Gln Gly
100          105          110
Thr Leu Val Thr Val Ser Ala
115

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...360

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAA GTG AAG ACT GAG GAG TCT GGA GGA GGC TTG GTT CAA CCT GGA GGA	48
Glu Val Lys Thr Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ACT TTC AGT AAC TAC	96
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr	
20 25 30	
TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT	144
Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val	
35 40 45	
GCT GAA ATT AGA TTG AAA TCT AAT AAT TAT GCA ACA CAT TAT GCG GAG	192
Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu	
50 55 60	
TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT AGT	240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser	
65 70 75 80	
GTC TAC CTG CAA ATG AAC AAC TTA AGA GCT GAA GAC ACT GGC ATT TAT	288
Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr	
85 90 95	
TAC TGT ACC CGT TAC GGT AGA GAG GGG GGG TTT GCT TAC TGG GGG GAA	336
Tyr Cys Thr Arg Tyr Gly Arg Glu Gly Gly Phe Ala Tyr Trp Gly Glu	
100 105 110	
GGG ACT CTG GTC ACT GTC TCT GCA	360
Gly Thr Leu Val Thr Val Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Glu Val Lys Thr Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20           25           30
Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35           40           45
Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu
 50           55           60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
 65           70           75           80
Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
 85           90           95
Tyr Cys Thr Arg Tyr Gly Arg Glu Gly Gly Phe Ala Tyr Trp Gly Glu
100           105           110
Gly Thr Leu Val Thr Val Ser Ala
115           120

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAA ACA ACT GTG ACC CAG TCT CCA GCA TCC CTG TCC GTG GCT ACA GGA	48
Glu Thr Thr Val Thr Gln Ser Pro Ala Ser Leu Ser Val Ala Thr Gly	
1 5 10 15	
GAA AAA GTC ACT ATC AGA TGC ATA ACC AGC ACT GAT ATT GAT GAT GAT	96
Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp	
20 25 30	
ATG AAC TGG TAC CAG CAG AAG CCA GGG GAA CCT CCT AAG CTC CTT ATT	144
Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile	
35 40 45	
TCA GAA GGC AAT ACT CTT CGT CCT GGA GTC CCA TCC CGA TTC TCC AGC	192
Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser	
50 55 60	
AGT GGC TAT GGC ACA GAT TTT GTT TTT ACA ATT GAA AAC ACG CTC TCA	240
Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Thr Leu Ser	
65 70 75 80	
GAA GAT GTT GCA GAT TAC TAC TGT TTG CAA AGT GAT AAC ATG CCT CTC	288
Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Met Pro Leu	
85 90 95	
ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG AAA	321
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu	Thr	Thr	Val	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Val	Ala	Thr	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Arg	Cys	Ile	Thr	Ser	Thr	Asp	Ile	Asp	Asp	Asp
		20						25				30			
Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile
	35						40				45				
Ser	Glu	Gly	Asn	Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser
	50					55				60					
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Val	Phe	Thr	Ile	Glu	Asn	Thr	Leu	Ser
65				70					75					80	
Glu	Asp	Val	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Met	Pro	Leu
			85						90					95	
Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC ACA TCA GTA GGA	48
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly	
1 5 10 15	
GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT GTG GGT ACT AAT	96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn	
20 25 30	
GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT AAA GCA CTG ATT	144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile	
35 40 45	
TAC TCG GCA TCC TAC CGG TAC AGT GGA GTC CCT GAT CGC TTC ACA GGC	192
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly	
50 55 60	
AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC GAT GTG CAG TCT	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Val Gln Ser	
65 70 75 80	
GAA GAC TTG GCA GAG TAT TTC TGT CAG CAA TAT AAC ATC TAT CCG CTC	288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu	
85 90 95	
ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG AAA	321
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1           5           10           15
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20           25           30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
 35           40           45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
 50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Val Gln Ser
 65           70           75           80
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85           90           95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100           105

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAA ACA ACT GTG ACC CAG TCT CCA GCA TCC CTG TCC GTG GCT ACA GGA	48
Glu Thr Thr Val Thr Gln Ser Pro Ala Ser Leu Ser Val Ala Thr Gly	
1 5 10 15	
GAA AAA GTC ACT ATC AGA TGC ATA ACC AGC ACT GAT ATT GAT GAT GAT	96
Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp	
20 25 30	
ATG AAC TGG TAC CAG CAG AAG CCA GGG GAA CCT CCT AAG CTC CTT ATT	144
Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile	
35 40 45	
TCA GAA GGC AAT ACT CTT CGT CCT GGA GTC CCA TCC CGA TTC TCC AGC	192
Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser	
50 55 60	
AGT GGC TAT GGC ACA GAT TTT GTT TTT ACA ATT GAA AAC ACG CTC TCA	240
Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Thr Leu Ser	
65 70 75 80	
GAA GAT GTT GCA GAT TAC TAC TGT TTG CAA AGT GAT AAC ATG CCA TTC	288
Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Met Pro Phe	
85 90 95	
ACG TTC GGC TCG GGG ACA AAG TTG GAA ATA AAA	321
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu	Thr	Thr	Val	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Val	Ala	Thr	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Arg	Cys	Ile	Thr	Ser	Thr	Asp	Ile	Asp	Asp	Asp
			20					25					30		
Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Ser	Glu	Gly	Asn	Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser
	50					55				60					
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Val	Phe	Thr	Ile	Glu	Asn	Thr	Leu	Ser
65				70					75					80	
Glu	Asp	Val	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Met	Pro	Phe
			85					90					95		
Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...345

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAG GTG CAG CTT GTT GAG TCT GGT GGA GGA TTG GTG CAG CCT AAA GGG	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Lys Gly	
1 5 10 15	
TCA TTG AAA CTC TCA TGT GCA GCC TCT GGA TTC ACC TTC AAT ACC TAC	96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr	
20 25 30	
GCC ATG AAC TGG GTC CGC CAG CTC CAA GGA AAG GGT TTG GAA TGG GTT	144
Ala Met Asn Trp Val Arg Gln Leu Gln Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCT CGC ATA AGA AGT AAA AGT AAT AAT TAT GCA ACA TAT TAT GCC GAT	192
Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp	
50 55 60	
TCA GTG AAA GAC AGG TTC ACC ATC TCC AGA GAT GAT TCA CAA AGC ATG	240
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Gln Ser Met	
65 70 75 80	
CTC TAT CTG CAA ATG AAC AAC TTG AAA ACT GAG GAC ACA GCC ATG TAT	288
Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr	
85 90 95	
TAC TGT GTG AGA CGG AGG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC	336
Tyr Cys Val Arg Arg Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr	
100 105 110	
GTC TCC TCA	345
Val Ser Ser	
115	

(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...372

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC TTG GTA CAG CCT GGG GGT	48
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC ACT GAT TAC	96
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp Tyr	
20 25 30	
TAC ATG AGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG	144
Tyr Met Ser Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu	
35 40 45	
GGT TTG ATT AGA AAC AAA GCT AAT GGT TAC ACA ACA GAG TAC AGT GCA	192
Gly Leu Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala	
50 55 60	
TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA GAT AAT TCC CAA AGC ATC	240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile	
65 70 75 80	
CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT GAG GAC AGT GCC ACT TAT	288
Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala Thr Tyr	
85 90 95	
TAC TGT GCA AGA GAT ATC TAC TAT GAT TAC GAC TAC TAT GCT ATG GAC	336
Tyr Cys Ala Arg Asp Ile Tyr Tyr Asp Tyr Asp Tyr Tyr Ala Met Asp	
100 105 110	
TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA	372
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE: internal
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp Tyr
          20           25           30
Tyr Met Ser Trp Val Arg Gln Pro Gly Lys Ala Leu Glu Trp Leu
          35           40           45
Gly Leu Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala
          50           55           60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile
          65           70           75           80
Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala Thr Tyr
          85           90           95
Tyr Cys Ala Arg Asp Ile Tyr Tyr Asp Tyr Asp Tyr Tyr Ala Met Asp
          100          105          110
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
          115          120

```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...111
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

CAC TGG AAC CAA CAG AAA CCA GGA CAG CCA CCC AGA CTC CTC ATC TAT      48
His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
 1           5           10           15

CTT GTA TCC AAC CTA GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC AGT      96
Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
          20           25           30

GGG TCT GGG ACA GAC      111
Gly Ser Gly Thr Asp
          35

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
 1           5           10
Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
      20           25           30
Gly Ser Gly Thr Asp
      35

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAAGATCTAG ACTTACTATG CAGCATCAGC

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGGAGACTAG TGGTTACTAA TTTGGAAGG ACTG

34

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAGACGACTA GTGGTGGCGG TGGCTCTCCA TTCGTTTGTG AATATCAA

48

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTACTAGCTA GCATAATAAC GGAATACCCA AAAGAACTGG

40

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TATGCTAGCT AGTAACACGA GAGGTTTCCC GACTGG

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AGCTTGAAT TCGTGAAATT GTTATCCGCT

30

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>17</u> , line <u>22</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 14 April 1993 (16.04.93)	Accession Number HB 11330
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
<div style="border: 1px solid black; padding: 5px;"><div style="text-align: center; font-weight: bold; font-size: small;">For receiving Office use only</div><div style="margin-top: 10px;"><input type="checkbox"/> This sheet was received with the international application</div><div style="border-top: 1px solid black; margin-top: 10px; height: 40px; vertical-align: bottom;">Authorized officer</div></div>	<div style="border: 1px solid black; padding: 5px;"><div style="text-align: center; font-weight: bold; font-size: small;">For International Bureau use only</div><div style="margin-top: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border-top: 1px solid black; margin-top: 10px; height: 40px; vertical-align: bottom;">Authorized officer</div></div>

~~RECTIFIED SHEET (RULE 91)~~

WHAT IS CLAIMED IS:

1. An isolated nucleic acid sequence coding for a heavy chain Fd fragment of a monoclonal antibody,
5 wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the nucleic acid sequence includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID
10 NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:17), 11D11 (SEQ ID NO:19), 14G11 (SEQ ID NO:21), 6F5 (SEQ ID NO:23), 7D10 (SEQ ID NO:25), 4E8 (SEQ ID NO:27), 2B4 (SEQ ID NO:35), or 2E7 (SEQ ID NO:37).
- 15 2. An isolated nucleic acid sequence coding for a light chain of a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the nucleic acid sequence includes the sequence for the light chain variable
20 region from monoclonal antibody 6B11 (SEQ ID NO:11), 1254 (SEQ ID NO:13), 14F11 (SEQ ID NO:15), 10G5 (SEQ ID NO:29), 2E7 (SEQ ID NO:31), or 7D10 (SEQ ID NO:33).
- 25 3. An expression cassette comprising:
a nucleic acid sequence coding for a heavy chain Fd fragment of a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, wherein the nucleic acid sequence
30 includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:17), 11D11 (SEQ ID NO:19), 14G11 (SEQ ID NO:21), 6F5
35 (SEQ ID NO:23), 7D10 (SEQ ID NO:25), 4E8 (SEQ ID NO:27), 2B4 (SEQ ID NO:35), or 2E7 (SEQ ID NO:37);

wherein the nucleic acid sequence coding for the heavy chain Fd fragment is operably linked to a promoter functional in a vector.

- 5 4. An expression cassette according to claim 3 further comprising a leader sequence located between the promoter and the nucleic acid sequence, wherein the leader sequence functions to direct the heavy chain Fd fragment to a membrane in a host cell.
- 10
5. An expression cassette comprising:
- (a) a nucleic acid sequence coding for a light chain for a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead
- 15 cation, wherein the nucleic acid sequence includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:11), 1254 (SEQ ID NO:13), 14F11 (SEQ ID NO:15), 10G5 (SEQ ID NO:29), 2E7 (SEQ ID NO:31), or 7D10 (SEQ ID NO:33),
- 20 wherein the nucleic acid sequence coding for the light chain is operably linked to a promoter functional in a vector.
6. An expression cassette according to claim 5 further comprising a leader sequence located between the
- 25 promoter and the nucleic acid sequence, wherein the leader sequence functions to direct the light chain to a membrane in a host cell.
- 30 7. An expression cassette coding for a fusion protein comprising:
- (a) a first nucleic acid sequence coding for a heavy chain Fd fragment of a monoclonal antibody, wherein the monoclonal antibody reacts
- 35 with lead cation, wherein the first nucleic acid sequence includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ

ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:17), 11D11 (SEQ ID NO:19), 14G11 (SEQ ID NO:21), 6F5 (SEQ ID NO:23), 7D10 (SEQ ID NO:25),
5 4E8 (SEQ ID NO:27), 2B4 (SEQ ID NO:35), or 2E7 (SEQ ID NO:37), and wherein the first nucleic acid sequence is linked for co-expression to

(b) a second nucleic acid sequence coding for a phage coat protein or a portion thereof; thereby forming a nucleic acid sequence encoding the fusion protein, wherein the fusion protein includes the heavy chain Fd fragment fused to the phage coat protein or portion thereof; and

(c) a promoter that is functional in a vector, wherein the promoter is operably linked to the first and second nucleic acid sequences and provides for expression of the fusion protein.

8. An expression cassette according to claim 7 further comprising a leader sequence located between the promoter and the nucleic acid sequence coding for the fusion protein, wherein the leader sequence directs expression of the fusion protein to a membrane of a host cell.

25

9. An expression cassette comprising:

(a) a first nucleic acid sequence coding for a heavy chain Fd fragment of a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, wherein the first nucleic acid sequence includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:17), 11D11 (SEQ ID NO:19), 14G11 (SEQ ID NO:21), 6F5 (SEQ ID NO:23),

35

7D10 (SEQ ID NO:25), 4E8 (SEQ ID NO:27), 2B4 (SEQ ID NO:35), or 2E7 (SEQ ID NO:37), and

wherein the first nucleic acid sequence is linked for co-expression to

5 (b) a second nucleic acid sequence for phage coat protein or a portion thereof to form a nucleic acid sequence encoding a fusion protein, wherein the fusion protein includes the heavy chain Fd fragment fused to the phage coat protein or
10 portion thereof;

(c) a first promoter that is functional in a vector, wherein the first promoter is operably linked to the nucleic acid sequence encoding the fusion protein and provides for expression of the
15 fusion protein; and

(d) a fourth nucleic acid sequence coding for a light chain of an antibody;

wherein the fourth nucleic acid sequence is operably linked to a second promoter functional
20 in the vector, and wherein the first and second promoters are coordinately expressed.

10. The expression cassette of claim 9, wherein the light chain is a light chain of a monoclonal
25 antibody which immunoreacts with a lead cation, and wherein the fourth nucleic acid sequence includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:11), 1254 (SEQ ID NO:13), 14F11 (SEQ ID NO:15), 10G5 (SEQ ID NO:29), 2E7 (SEQ ID NO:31), or 7D10 (SEQ ID NO:33).
30

11. A phagemid vector having the expression cassette of claim 9.
35

12. A metal binding polypeptide comprising an amino acid sequence for a heavy chain Fd fragment from a

monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the amino acid sequence for the heavy chain Fd fragment includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:2), 1254 (SEQ ID NO:4), 8E7 (SEQ ID NO:6), 10G5 (SEQ ID NO:8), 14F11 (SEQ ID NO:10), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5 (SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO:38).

13. The polypeptide of claim 12 further comprising a heavy chain Fc fragment fused to the heavy chain Fd fragment.

14. The polypeptide of claim 12 further comprising a phage coat protein or portion thereof fused to the heavy chain Fd fragment.

15. A heavy chain of a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the heavy chain has an amino acid sequence which includes the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:2), 1254 (SEQ ID NO:4), 8E7 (SEQ ID NO:6), 10G5 (SEQ ID NO:8), 14F11 (SEQ ID NO:10), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5 (SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO: 38).

16. A fusion protein comprising a heavy chain Fd fragment of a monoclonal antibody and a phage coat protein or portion thereof, wherein the monoclonal antibody immunoreacts with a lead cation.

17. A phage comprising a fusion protein according to claim 16 and a light chain of an antibody.
18. The phage of claim 17 wherein the light chain is a light chain of a monoclonal antibody which immunoreacts with the lead cation.
19. A metal binding polypeptide comprising an amino acid sequence for a light chain from a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the light chain amino acid sequence includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:12), 1254 (SEQ ID NO:14), 14F11 (SEQ ID NO:16), 10G5 (SEQ ID NO:30), 2E7 (SEQ ID NO:32), or 7D10 (SEQ ID NO:34).
20. A light chain of a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and wherein the light chain has an amino acid sequence which includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:12), 1254 (SEQ ID NO:14), 14F11 (SEQ ID NO:16), 10G5 (SEQ ID NO:30), 2E7 (SEQ ID NO:32), or 7D10 (SEQ ID NO:34).
21. A recombinantly produced Fab fragment that immunoreacts with a lead cation, wherein the Fab fragment has a heavy chain Fd fragment with an amino acid sequence which includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:2), 1254 (SEQ ID NO:4), 8E7 (SEQ ID NO:6), 10G5 (SEQ ID NO:8), 14F11 (SEQ ID NO:10), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5 (SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO: 38).

22. A recombinantly produced Fab fragment that immunoreacts with a lead cation, the Fab fragment comprising a light chain having an amino acid sequence which includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:12), 1254 (SEQ ID NO:14), 14F11 (SEQ ID NO:16), 10G5 (SEQ ID NO:30), 2E7 (SEQ ID NO:32), or 7D10 (SEQ ID NO:34).
23. A purified antibody comprising a Fab fragment that immunoreacts with a lead cation, the Fab fragment comprising a heavy chain Fd fragment having an amino acid sequence which includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:2), 1254 (SEQ ID NO:4), 8E7 (SEQ ID NO:6), 10G5 (SEQ ID NO:8), 14F11 (SEQ ID NO:10), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5 (SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO:38).
24. The purified antibody of claim 23 which is a recombinantly produced monoclonal antibody.
25. A purified antibody comprising a Fab fragment that immunoreacts with a lead cation, the Fab fragment comprising a light chain having an amino acid sequence which includes the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:12), 1254 (SEQ ID NO:14), 14F11 (SEQ ID NO:16), 10G5 (SEQ ID NO:30), 2E7 (SEQ ID NO:32), or 7D10 (SEQ ID NO:34).
26. A kit for detecting the presence of lead cations comprising a metal binding polypeptide which includes an amino acid sequence for a heavy chain Fd fragment from a monoclonal antibody, wherein the

monoclonal antibody immunoreacts with a lead cation, and the heavy chain Fd fragment has an amino acid sequence which includes the sequence for the heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:2), 1254 (SEQ ID NO:4), 8E7 (SEQ ID NO:6), 10G5 (SEQ ID NO:8), 14F11 (SEQ ID NO:10), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5 (SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO:38).

27. A kit for detecting the presence of lead cations comprising a metal binding polypeptide which includes an amino acid sequence for a light chain from a monoclonal antibody, wherein the monoclonal antibody immunoreacts with a lead cation, and the light chain has an amino acid sequence including the sequence for the light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:12), 1254 (SEQ ID NO:14), 14F11 (SEQ ID NO:16), 10G5 (SEQ ID NO:30), 2E7 (SEQ ID NO:32), or 7D10 (SEQ ID NO:34).

28. A method of producing a metal binding polypeptide comprising:

i) expressing a nucleic acid sequence in a transformed host cell to form a lead binding polypeptide, said nucleic acid sequence comprises a sequence coding for a heavy chain Fd fragment of a monoclonal antibody which is capable of immunoreacting with a lead cation, wherein the sequence coding for the heavy chain Fd fragment includes a sequence for a heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:18), 11D11 (SEQ ID NO:20), 14G11 (SEQ ID NO:22), 6F5

(SEQ ID NO:24), 7D10 (SEQ ID NO:26), 4E8 (SEQ ID NO:28), 2B4 (SEQ ID NO:36), or 2E7 (SEQ ID NO:38).

29. The method of claim 28 wherein the metal binding polypeptide is a fusion protein and the sequence coding for the heavy chain Fd fragment is linked for co-expression to a nucleic acid sequence coding for an adjunct peptide.
30. A method of producing a metal binding polypeptide comprising:
expressing a nucleic acid sequence in a transformed host cell to form a lead binding polypeptide, said nucleic acid sequence comprising a sequence coding for a light chain of a monoclonal antibody which is capable of immunoreacting with a lead cation, wherein the sequence coding for the light chain includes a sequence encoding a light chain variable region from monoclonal antibody 6B11 (SEQ ID NO:11), 1254 (SEQ ID NO:13), 14F11 (SEQ ID NO:15), 10G5 (SEQ ID NO:29), 2E7 (SEQ ID NO:31), or 7D10 (SEQ ID NO:33).
31. A metal binding polypeptide obtainable by a process comprising:
expressing a nucleic acid sequence in a transformed host cell, wherein the nucleic acid sequence consists essentially of a sequence coding for a heavy chain variable region from monoclonal antibody 6B11 (SEQ ID NO:1), 1254 (SEQ ID NO:3), 8E7 (SEQ ID NO:5), 10G5 (SEQ ID NO:7), 14F11 (SEQ ID NO:9), 13D10 (SEQ ID NO:17), 11D11 (SEQ ID NO:19), 14G11 (SEQ ID NO:21), 6F5 (SEQ ID NO:23), 7D10 (SEQ ID NO:25), 4E8 (SEQ ID NO:27), 2B4 (SEQ ID NO:35), or 2E7 (SEQ ID NO:37).
32. A method of producing a metal binding antibody specific for a metallic cation comprising injecting

an antibody capable of immunoreacting with the metallic cation into a mammal.

- 5 33. The method of claim 32 wherein the metallic cation is a cation of lead or mercury.
- 10 34. A hybridoma of myeloma immortal cells and mammalian immune cells from a mammal previously immunized with a first antibody capable of immunoreacting with a metallic cation, wherein the hybridoma produces a second monoclonal antibody capable of immunoreacting with the metallic cation in an exposed state.
- 15 35. A lead binding polypeptide comprising a light chain of a monoclonal antibody capable of immunoreacting with a lead cation.
- 20 36. The polypeptide of claim 35 wherein the light chain is a member of the V_L32 light chain family.
- 25 37. The polypeptide of claim 35 wherein the light chain comprises a motif of five consecutive amino acid residues, where four of the five amino acid residues each have a carboxylic acid-containing side chain.
- 30 38. The polypeptide of claim 37 wherein the motif is present in a CDR1 region of the light chain.
39. The polypeptide of claim 38 wherein the motif is positioned at amino acid residues 28, 29, 30 31 and 32.
- 35 40. The polypeptide of claim 37 wherein the amino acid residues having a carboxylic acid-containing side chain are glutamic acid or aspartic acid.

41. An isolated nucleic acid sequence coding for a light chain of a monoclonal antibody capable of immunoreacting with a lead cation, wherein the monoclonal antibody is a member of the V_κ32 light chain family.
- 5

1/13

Sequences of Heavy Chains of Lead-Specific Antibodies

FIG. 1A

	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960	4970	4980	4990	5000	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400	5410	5420	5430	5440	5450	5460	5470	5480	5490	5500	5510	5520	5530	5540	5550	5560	5570	5580	5590	5600	5610	5620	5630	5640	5650	5660	5670	5680	5690	5700	5710	5720	5730	5740	5750	5760	5770	5780	5790	5800	5810	5820	5830	5840	5850	5860	5870	5880	5890	5900	5910	5920	5930	5940	5950	5960	5970	5980	5990	6000	6010	6020	6030	6040	6050	6060	6070	6080	6090	6100	6110	6120	6130	6140	6150	6160	6170	6180	6190	6200	6210	6220	6230	6240	6250	6260	6270	6280	6290	6300	6310	6320	6330	6340	6350	6360	6370	6380	6390	6400	6410	6420	6430	6440	6450	6460	6470	6480	6490	6500	6510	6520	6530	6540	6550	6560	6570	6580	6590	6600	6610	6620	6630	6640	6650	6660	6670	6680	6690	6700	6710	6720	6730	6740	6750	6760	6770	6780	6790	6800	6810	6820	6830	6840	6850	6860	6870	6880	6890	6900	6910	6920	6930	6940	6950	6960	6970	6980	6990	7000	7010	7020	7030	7040	7050	7060	7070	7080	7090	7100	7110	7120	7130	7140	7150	7160	7170	7180	7190	7200	7210	7220	7230	7240	7250	7260	7270	7280	7290	7300	7310	7320	7330	7340	7350	7360	7370	7380	7390	7400	7410	7420	7430	7440	7450	7460	7470	7480	7490	7500	7510	7520	7530	7540	7550	7560	7570	7580	7590	7600	7610	7620	7630	7640	7650	7660	7670	7680	7690	7700	7710	7720	7730	7740	7750	7760	7770	7780	7790	7800	7810	7820	7830	7840	7850	7860	7870	7880	7890	7900	7910	7920	7930	7940	7950	7960	7970	7980	7990	8000	8010	8020	8030	8040	8050	8060	8070	8080	8090	8100	8110	8120	8130	8140	8150	8160	8170	8180	8190	8200	8210	8220	8230	8240	8250	8260	8270	8280	8290	8300	8310	8320	8330	8340	8350	8360	8370	8380	8390	8400	8410	8420	8430	8440	8450	8460	8470	8480	8490	8500	8510	8520	8530	8540	8550	8560	8570	8580	8590	8600	8610	8620	8630	8640	8650	8660	8670	8680	8690	8700	8710	8720	8730	8740	8750	8760	8770	8780	8790	8800	8810	8820	8830	8840	8850	8860	8870	8880	8890	8900	8910	8920	8930	8940	8950	8960	8970	8980	8990	9000	9010	9020	9030	9040	9050	9060	9070	9080	9090	9100	9110	9120	9130	9140	9150	9160	9170	9180	9190	9200	9210	9220	9230	9240	9250	9260	9270	9280	9290	9300	9310	9320	9330	9340	9350	9360	9370	9380	9390	9400	9410	9420	9430	9440	9450	9460	9470	9480	9490	9500	9510	9520	9530	9540	9550	9560	9570	9580	9590	9600	9610	9620	9630	9640	9650	9660	9670	9680	9690	9700	9710	9720	9730	9740	9750	9760	9770	9780	9790	9800	9810	9820	9830	9840	9850	9860	9870	9880	9890	9900	9910	9920	9930	9940	9950	9960	9970	9980	9990	10000	10010	10020	10030	10040	10050	10060	10070	10080	10090	10100	10110	10120	10130	10140	10150	10160	10170	10180	10190	10200	10210	10220	10230	10240	10250	10260	10270	10280	10290	10300	10310	10320	10330	10340	10350	10360	10370	10380	10390	10400	10410	10420	10430	10440	10450	10460	10470	10480	10490	10500	10510	10520	10530	10540	10550	10560	10570	10580	10590	10600	10610	10620	10630	10640	10650	10660	10670	10680	10690	10700	10710	10720	10730	10740	10750	10760	10770	10780	10790	10800	10810	10820	10830	10840	10850	10860	10870	10880	10890	10900	10910	10920	10930	10940	10950	10960	10970	10980	10990	11000	11010	11020	11030	11040	11050	11060	11070	11080	11090	11100	11110	11120	11130	11140	11150	11160	11170	11180	11190	11200	11210	11220	11230	11240	11250	11260	11270	11280	11290	11300	11310	11320	11330	11340	11350	11360	11370	11380	11390	11400	11410	11420	11430	11440	11450	11460	11470	11480	11490	11500	11510	11520	11530	11540	11550	11560	11570	11580	11590	11600	11610	11620	11630	11640	11650	11660	11670	11680	11690	11700	11710	11720	11730	11740	11750	11760	11770	11780	11790	11800	11810	11820	11830	11840	11850	11860	11870	11880	11890	11900	11910	11920	11930	11940	11950	11960	11970	11980	11990	12000	12010	12020	12030	12040	12050	12060	12070	12080	12090	12100	12110	12120	12130	12140	12150	12160	12170	12180	12190	12200	12210	12220	12230	12240	12250	12260	12270	12280	12290	12300	12310	12320	12330	12340	12350	12360	12370	12380	12390	12400	12410	12420	12430	12440	12450	12460	12470	12480	12490	12500	12510	12520	12530	12540	12550	12560	12570	12580	12590	12600	12610	12620	12630	12640	12650	12660	12670	12680	12690	12700	12710	12720	12730	12740	12750	12760	12770	12780	12790	12800	12810	12820	12830	12840	12850	12860	12870	12880	12890	12900	12910	12920	12930	12940	12950	12960	12970	12980	12990	13000	13010	13020	13030	13040	13050	13060	13070	13080	13090	13100	13110	13120	13130	13140	13150	13160	13170	13180	13190	13200	13210	13220	13230	13240	13250	13260
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Sequences of Heavy Chains of Lead-Specific Antibodies

6811	110	Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
		TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA
1286		Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
		TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA
887		Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
		TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
1085		Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
		TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA
14711		Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
		TGG GGC GCA GGG ACC ACC GTC ACC GTC TCC TCA

FIG. 1B

SUBSTITUTE SHEET (RULE 26)

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Sequences of Light Chain Variable Regions of Lead-Specific Antibodies

	COR1										COR2										COR3																																							
	20										30										40										50										60										70									
6B11	Thr	Gln	Ser	Pro	Ser	Leu	Ser	Met	Ala	Ile	Gly	Glu	Lys	Val	Thr	Ile	Arg	Cys	Ile	Thr	Ser	Thr	Arg	Ile	Asp	Asp	Met	Asn	Trp	Tyr	Gln																													
	ACC	CAG	TCT	CCA	TCA	TCC	ATG	GCT	ATA	GAA	AAA	ATC	ACC	ATC	AGA	TGC	ATA	ACC	AGC	AGT	GAT	GAT	GAT	GAT	GAT	GAT	ATG	ATC	TGG	TAC	CAG																													
1254	Thr	Gln	Ser	Pro	Ser	Leu	Ser	Met	Ala	Ile	Gly	Glu	Lys	Val	Thr	Ile	Arg	Cys	Ile	Thr	Ser	Thr	Arg	Ile	Asp	Asp	Met	Asn	Trp	Tyr	Gln																													
																													
14711	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Met	Ala	Ile	Gly	Glu	Lys	Val	Thr	Ile	Arg	Cys	Ile	Thr	Ser	Thr	Arg	Ile	Asp	Asp	Met	Asn	Trp	Tyr	Gln																												
																													
6B11	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile	Ser	Glu	Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Val	Thr																										
	CAG	AAG	CCA	CGG	GAA	CCT	CCT	AAA	CTC	CTT	ATT	TCA	GAA	GAC	AAT	CTT	CGT	CGA	CTC	CCA	TCC	AGC	AGT	GGC	TAT	GGT	ACA	GAT	TTT	ATT	TTT	ACA																												
1254	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile	Ser	Glu	Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Val	Thr																										
																											
14711	Gln	Lys	Pro	Gly	Glu	Pro	Pro	Lys	Leu	Leu	Ile	Ser	Glu	Thr	Leu	Arg	Pro	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ser	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Val	Thr																										
																										
6B11	Ile	Glu	Asn	Met	Leu	Ser	Glu	Asp	Val	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Leu	Pro	Leu	Thr	Phe	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg																											
	ATT	GAA	AAC	ATG	CTC	TCA	GAA	GAT	GAT	GAT	GAT	TAC	TAC	TAT	TTC	CAA	AAT	GAT	AAC	TTC	CTT	CTC	AGC	TTC	CGA	GGG	GGG	ACC	AGC	AGC	ATA	AAA	CGG																											
1254	Ile	Glu	Asn	Met	Leu	Ser	Glu	Asp	Val	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Leu	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg																										
																										
14711	Ile	Glu	Asn	Met	Leu	Ser	Glu	Asp	Val	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Ser	Asp	Asn	Leu	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg																										
																										

FIG. 2

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Lead-Specific Heavy Chain Sequences									
	80	82	82A	82B	82C	83	90	94	103
11D10	Asp Thr Ser Lys Asn Gln Phe Leu Gln Phe Leu Gln Leu Asn Ser Val Thr Thr Gln Asp Thr Thr Tyr Tyr Cys Ala Arg Cys Gly Asn Tyr Pro Trp Tyr Phe Asp Tyr Trp GAC ACA TCC AAG AAC CAG TTC TTC CTG CAG TTG AAT TCT GTG ACT ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TGT GGT AAC TAC CCG TGG TAC TTT GAC TAC TGG								
11D11	Asp Thr Ser Ser Asn Thr Ala Tyr Met Gln Val Ser Ser Leu Thr Ser Gln Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ile Tyr Tyr Gly His Leu Trp Phe Ala Tyr Trp GAT ACA TCC TCC AAC ACA GCC TAC ATG CAA GTC AGC AGC CTG ACA TCT GAG GAC TCT GCC GTC TAT TAC TGT GCA AGG ATC TAC TAT GGT CAC TTG TGG TTT GCT TAC TGG								
14G11	Asp Thr Ser Ser Asn Ile Ala Tyr Met Gln Leu Ser Ser Gln Asp Thr Thr Ala Val Tyr Tyr Cys Asn Pro Tyr Gln Tyr Asp Asp Ala Met Asp Tyr Trp GAC ACA TCC TCC AAT ATA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAT ACT GTC TAT TAC TGT AAT CCC TAT GGT TAC GAC GAT GCT ATG GAC ... TAC TGG								
6F5	Ser Arg Asp Ser Gln Ser Met Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Gln Asp Thr Ala Met Tyr Tyr Cys Val Arg Arg ... Phe Ala Tyr Trp TCC AGA GAT GAT TCA CAA AGC ATG CTC TAT CTG CAA ATG AAC TTTG AAA ACT GAG GAC ACA GCC ATG TAT TAC TGT GTG AGA CCG ... TTT GCT TAC TGG								
7D10	Arg Asp Ser Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Gln Asp Thr Thr Tyr Cys Thr Arg Tyr Gln Gln Gln Gln Val Ala Tyr Trp AGA GAT GAT TCC AAA AAT AGT GTC TAC CTG CAA ATG AAC TTA AGA OCT GAA GAC ACT GGA AAT TAT TAC TGT ACC GGT TAC GGT AGA GAG GCG GGT GCT TAC TGG								
4B8	Arg Asp Ser Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Gln Asp Thr Thr Tyr Cys Thr Arg Tyr Gln Gln Gln Gln Val Ala Tyr Trp AGA GAT GAT TCC AAA AAT AGT GTC TAC CTG CAA ATG AAC TTA AGA OCT GAA GAC ACT GGA AAT TAT TAC TGT ACC GGT TAC GGT AGA GAG GCG GGT GCT TAC TGG								
11D10	Gly Gln Gly Thr Thr Leu Thr Val Ser Ser GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA								
11D11	Gly Gln Gly Thr Leu Val Thr Val Ser Ala GGC CAA GCG ACT CTG GTC ACT GTC TCT GCA								
14G11	Gly Gln Gly Thr Ser Val Thr Val Ser Ser GGA CAA GGA ACC TCA GTC ACC GTC TCC TCA								
6F5	Gly Gln Gly Thr Leu Val Thr Val Ser Ala GGC CAA GCG ACT CTG GTC ACT GTC TCT GCA								
7D10	Gly Gln Gly Thr Leu Val Thr Val Ser Ala GGG CAA GCG ACT CTG GTC ACT GTC TCT GCA								
4B8	Gly Gln Gly Thr Leu Val Thr Val Ser Ala GGG GAA GCG ACT CTG GTC ACT GTC TCT GCA								

FIG. 3B

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FIG. 5

2B4 heavy chain

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                                10                                20
E V Q L V E S G G G L V Q P K G S L K L
GAG GTG CAG CTT GTT GAG TCT GGT GGA GGA TTG GTG CAG CCT AAA GGG TCA TTG AAA CTC

                                30                                40
S C A A S G P T F N T Y A M N W V R Q L
TCA TGT GCA GCC TCT GGA TTC ACC TTC AAT ACC TAC GCC ATG AAC TGG GTC CGC CAG CTC

                                50                                52 52A 52B 52C
Q G K G L E W V A R I R S K S N N Y A T
CAA GGA AAG GGT TTG GAA TGG GTT GCT CGC ATA AGA AGT AAA AGT AAT AAT TAT GCA ACA

                                60                                70
Y Y A D S V K D R F T I S R D D S Q S M
TAT TAT GCC GAT TCA GTG AAA GAC AGG TTC ACC ATC TCC AGA GAT GAT TCA CAA AGC ATG

                                80                                90
L Y L Q M N N L K T E D T A M Y Y C V R
CTC TAT CTG CAA ATG AAC AAC TTG AAA ACT GAG GAC ACA GCC ATG TAT TAC TGT GTG AGA

                                96                                101                                110
R R D Y W G Q G T S V T V S S
CGG AGG ... .. GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA

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FIG. 6

2E7 heavy chain

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC TTG GTA CAG CCT GGG GGT TCT CTG AGA CTC

Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Ser Trp Val Arg Gln Pro
TCC TGT GCA ACT TCT GGG TTC ACC TTC ACT GAT TAC TAC ATG AGC TGG GTC CGC CAG CCT

Pro Gly Lys Ala Leu Glu Trp Leu Gly Leu Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr
CCA GGA AAG GCA CTT GAG TGG TTG GGT TTG ATT AGA AAC AAA GCT AAT GGT TAC ACA ACA

Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile
GAG TAC AGT GCA TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA GAT AAT TCC CAA AGC ATC

Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg
CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT GAG GAC AGT GCC ACT TAT TAC TGT GCA AGA

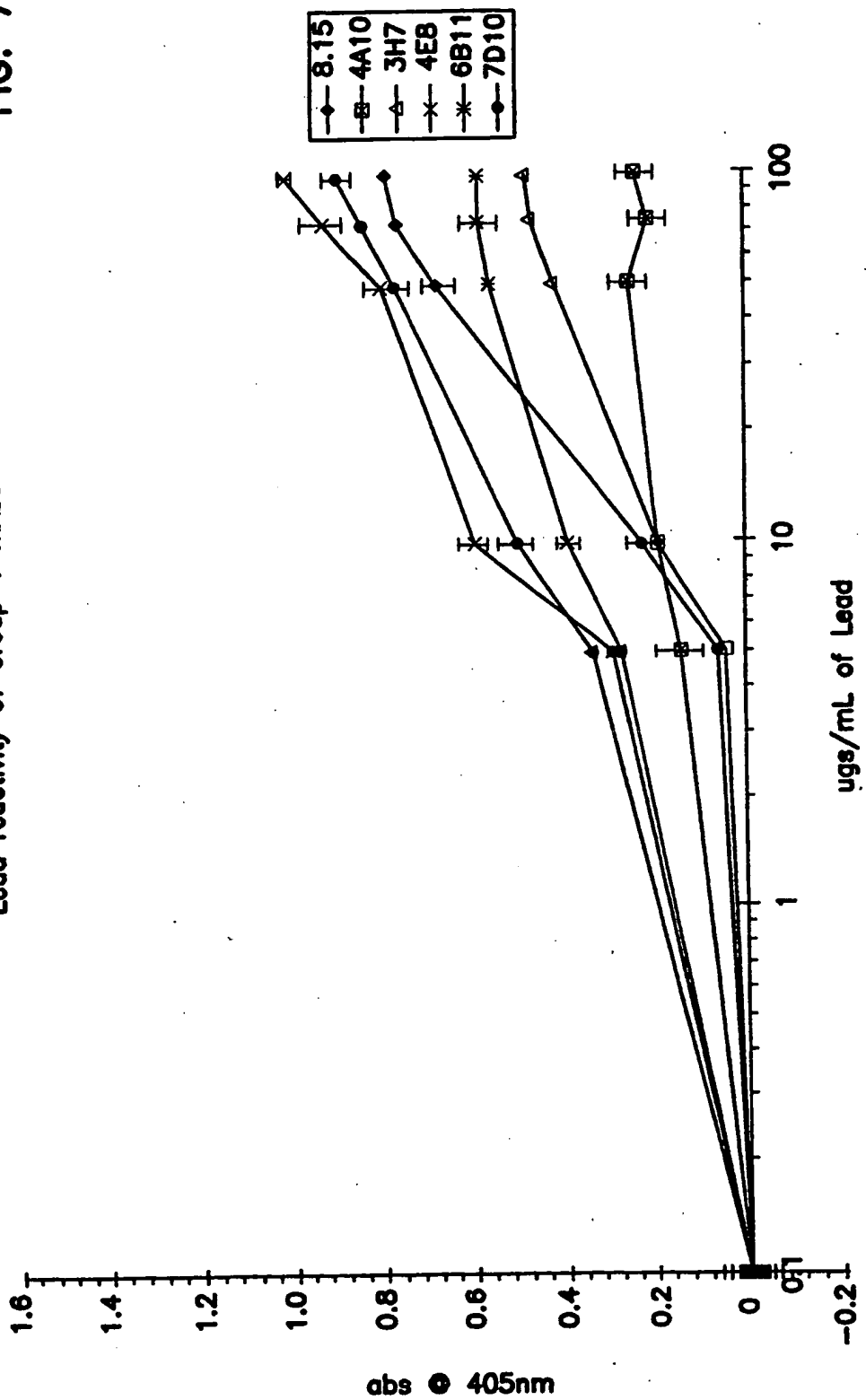
Asp Ile Tyr Tyr Asp Tyr Asp Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
GAT ATC TAC TAT GAT TAC GAC TAC TAT GCT ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC

Thr Val Ser Ser
ACC GTC TCC TCA

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FIG. 7

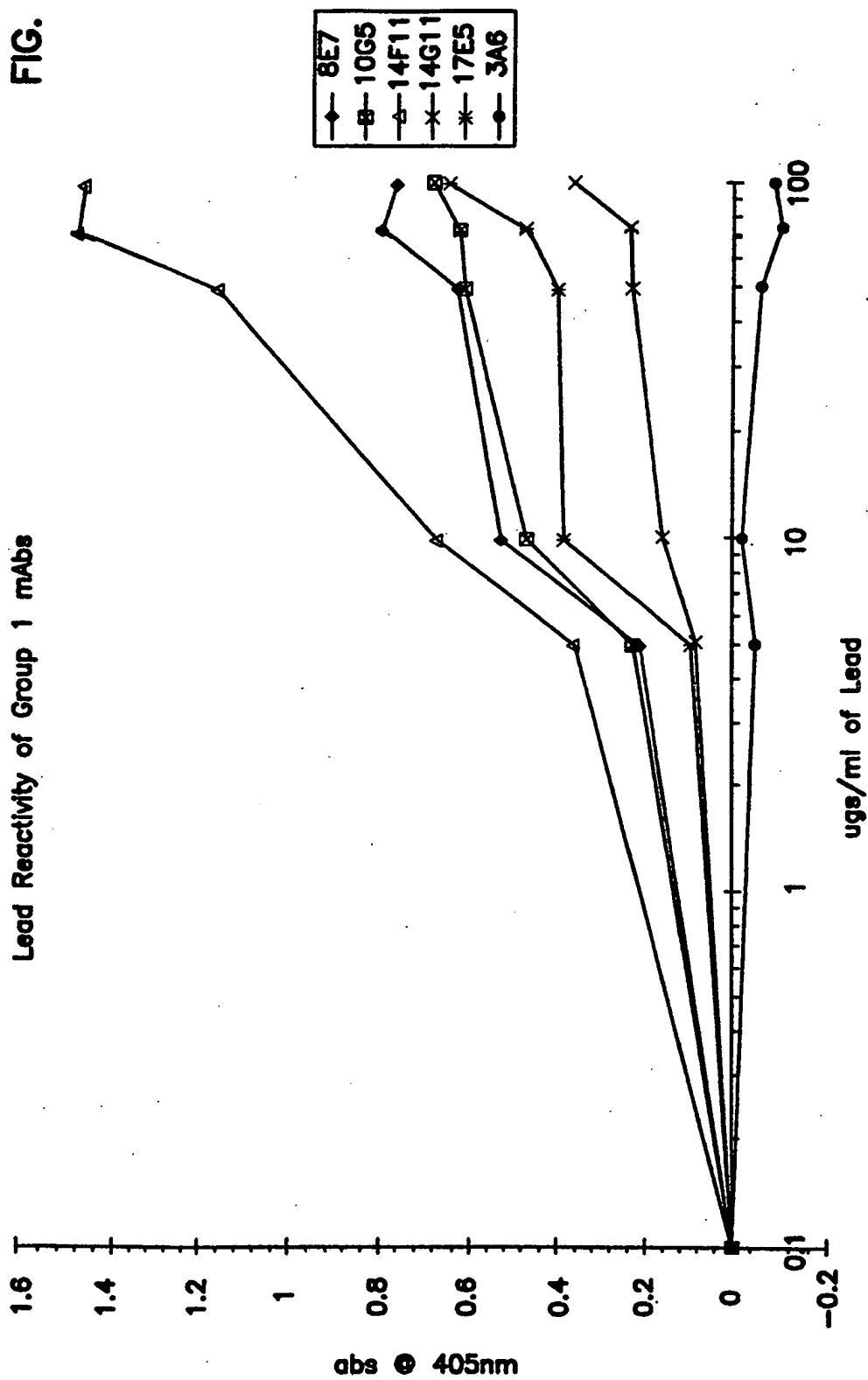
Lead reactivity of Group 1 mAbs



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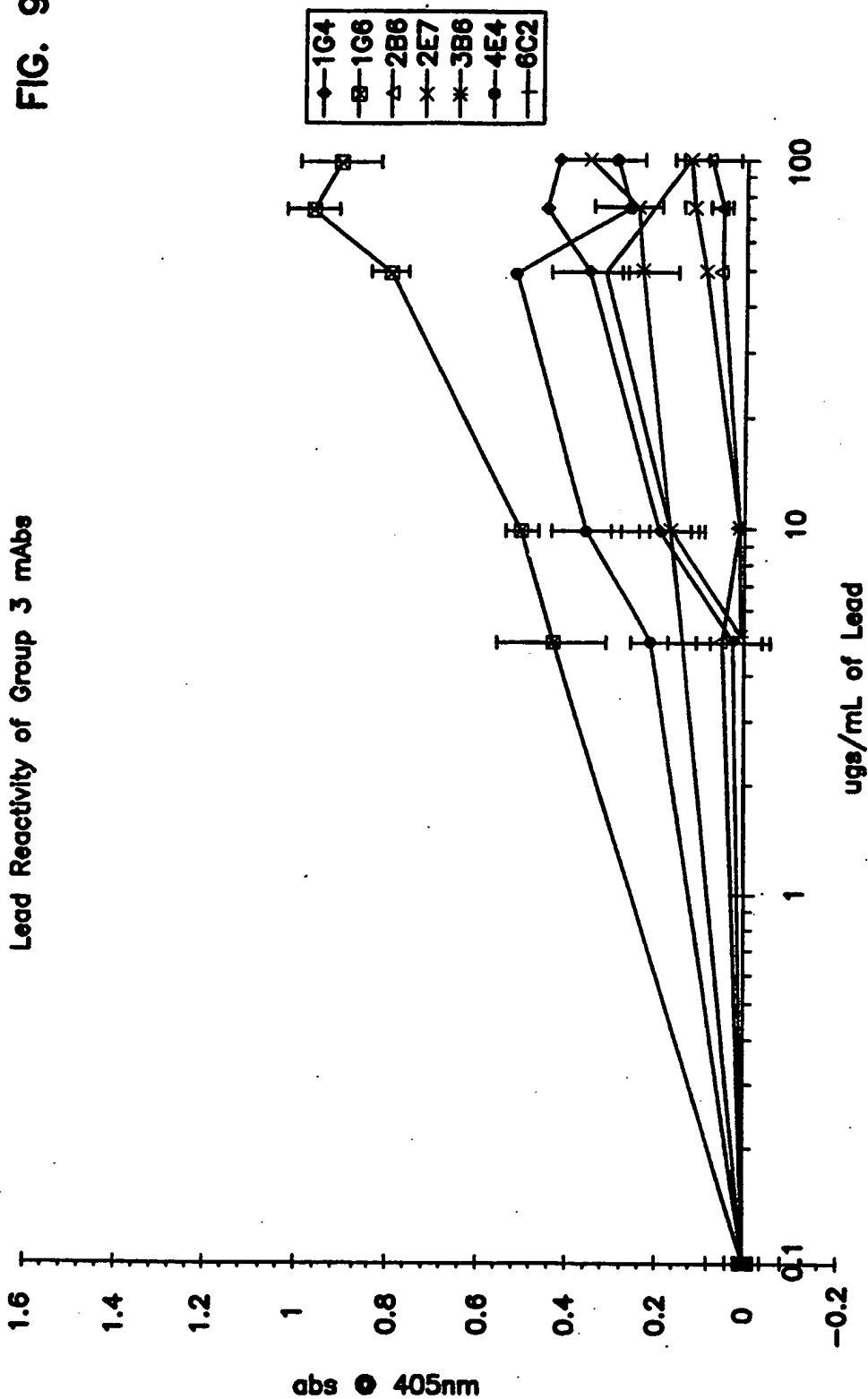
FIG. 8



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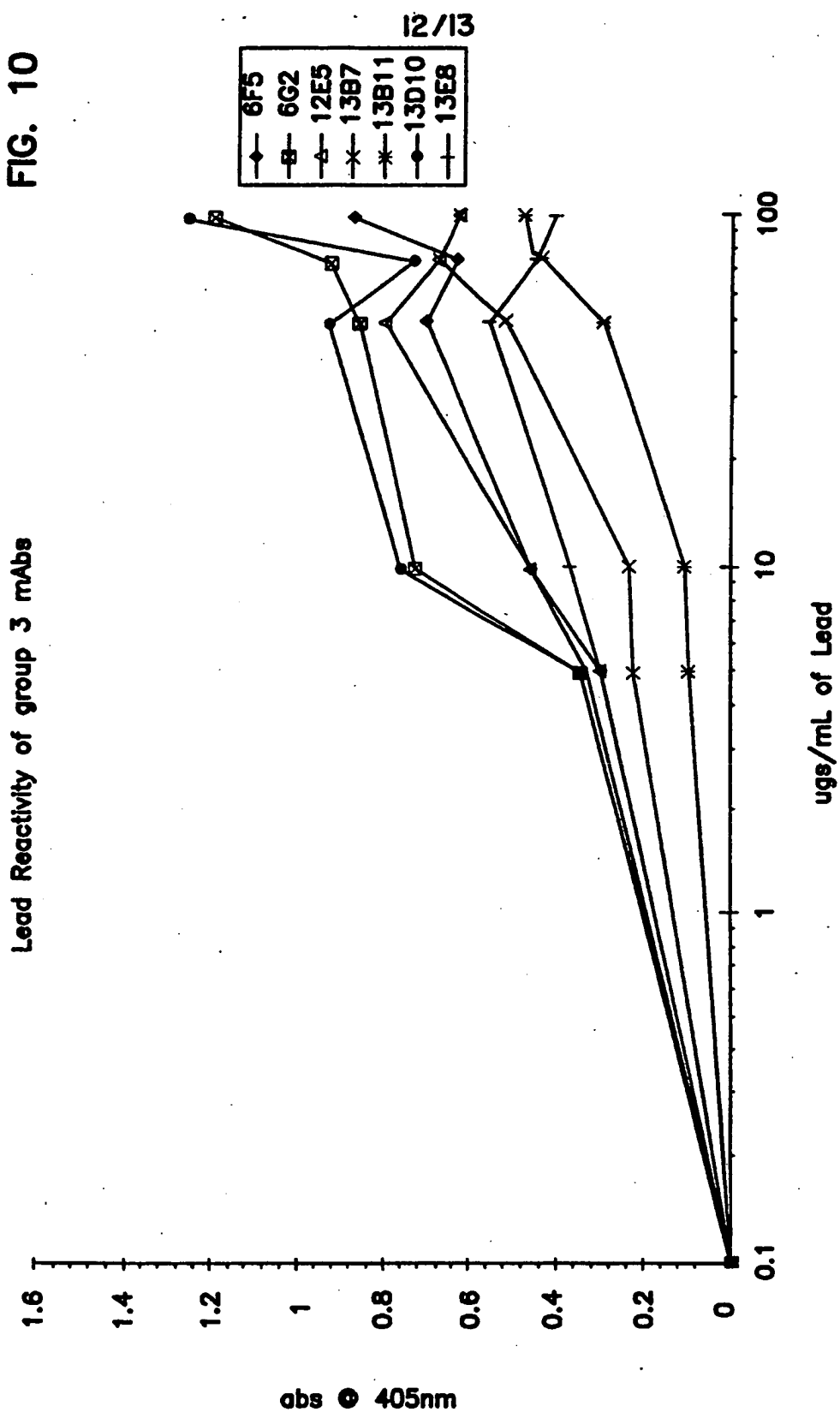
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FIG. 9



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FIG. 10

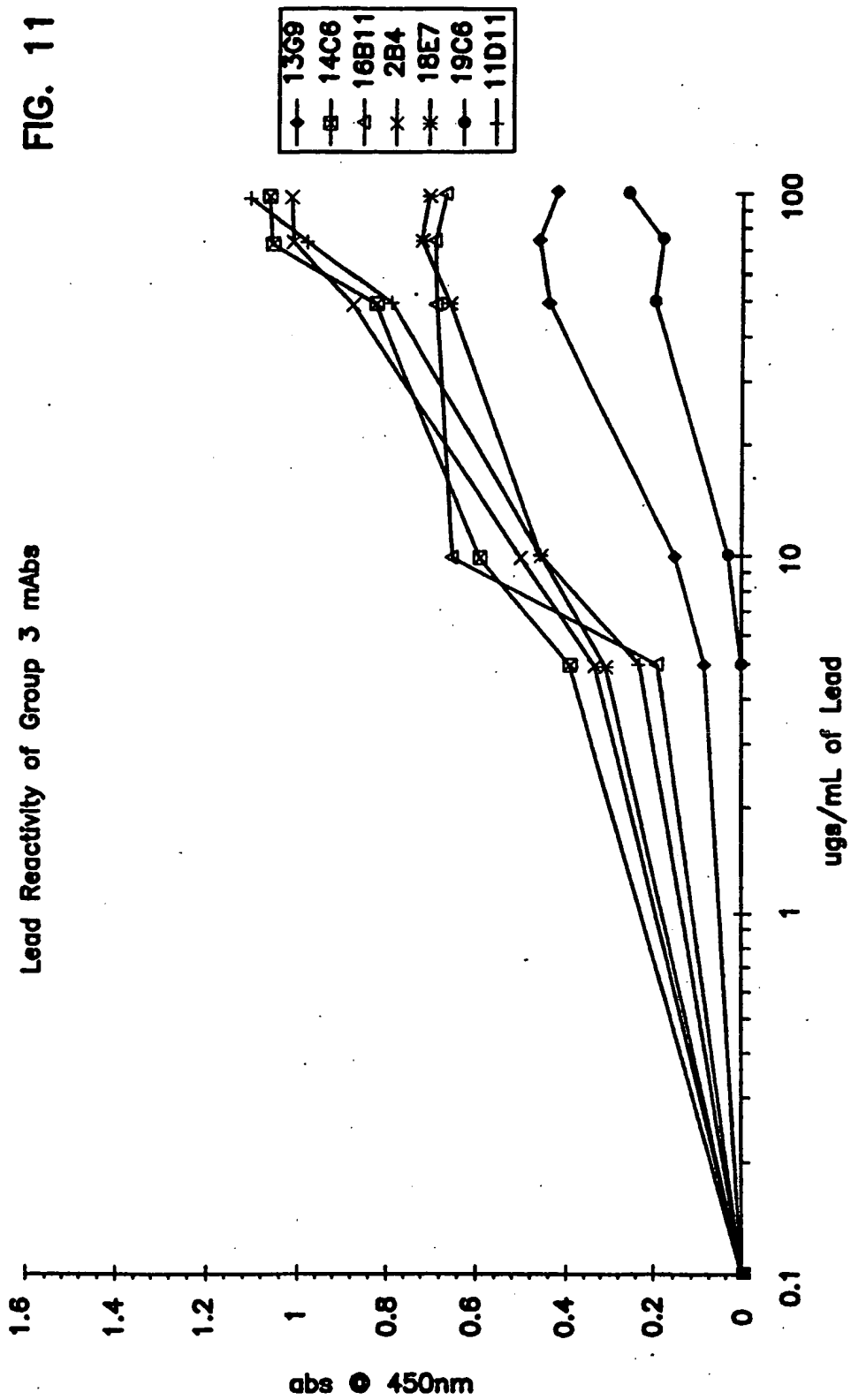


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FIG. 11

Lead Reactivity of Group 3 mAbs



SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

Int. Application No

PCT/US 96/09258

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/13 C07K16/44 C07K19/00 C12N15/62 G01N33/577
 G01N33/53 C12N5/20

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,94 18220 (SCRIPPS RESEARCH INST) 18 August 1994 see page 25 - page 26 ---	35-41
X	WO,A,90 10709 (UNIV NEBRASKA) 20 September 1990 see page 45 - page 46 ---	32-36,41
X	PROC NATL ACAD SCI U S A, MAY 1 1992, 89 (9) P4104-8, UNITED STATES, XP000601648 WYLIE DE ET AL: "Monoclonal antibodies specific for mercuric ions." see figure 1 ---	32-34
P,X	WO,A,95 18156 (ABBOTT LAB) 6 July 1995 see the whole document ---	32-35
	-/--	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

19 September 1996

Date of mailing of the international search report

02.10.96

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl;
 Fax: (+31-70) 340-3016

Authorized officer

Espen, J

INTERNATIONAL SEARCH REPORT

Int. Application No

PCT/US 96/09258

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL entry MM23047 Accession number U23047, 16 April 1995 JANG Y ET AL: "Heavy chain dominance in the binding of native DNA by a lupus mouse monoclonal autoantibody" XP002013728 see the whole document</p>	2,5,10, 19,20, 22,25, 27,30,32
X	<p>& IMMUNOLOGY LETTERS, vol. 14, 1986 - 1987, pages 53-58, XP000601123 KUBOTA T ET AL: "A monoclonal anti-double stranded DNA antibody from an autoimmune MRL/Mp-lpr/lpr mouse: specificity and idiotypic in serum immunoglobulins" see the whole document</p>	2,5,10, 19,20, 22,25, 27,30,32
X	<p>--- JOURNAL OF IMMUNOLOGY, vol. 136, 1986, BALTIMORE US, pages 1864-1870, XP000601650 DZIERZAK E A ET AL: "Molecular characterization of antibodies bearing Id-460" see the whole document</p>	1,3,7,9, 12,15, 21,23, 26,28,31
A	<p>--- BIOCHEM BIOPHYS RES COMMUN, FEB 28 1989, 159 (1) P177-84, UNITED STATES, XP000601647 DUVAL G ET AL: "Preliminary purification and characterization studies of a low molecular weight, high affinity cytosolic lead-binding protein in rat brain." see the whole document</p>	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/09258

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Please see Further Information sheet enclosed.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US96/09258

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

Remark: Although claims 32, 33 are directed to a method of treatment of (diagnostic method practised on) the human/animal body the search has been carried out and based on the alleged effects of the compound/composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 96/09258

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9418220	18-08-94	AU-A- 6132994	29-08-94
		AU-A- 6170394	29-08-94
		AU-A- 6235294	29-08-94
		WO-A- 9418219	18-08-94
		WO-A- 9418221	18-08-94

WO-A-9010709	20-09-90	AU-B- 648022	14-04-94
		AU-A- 5411490	09-10-90
		CA-A- 2047717	15-09-90
		EP-A- 0463110	02-01-92
		EP-A- 0589487	30-03-94
		JP-T- 5504464	15-07-93
		US-A- 5503987	02-04-96

WO-A-9518156	06-07-95	US-A- 5476939	19-12-95
		AU-A- 1406195	17-07-95
		CA-A- 2178642	06-07-95
